

Result No.	Score	Query Match	Length	DB ID	Description
1	1720	100.0	317	20 AAV06482	Human tumour-assoc Amino acid sequenc
2	1720	100.0	317	20 AAV13391	Human serine prote
3	1720	100.0	317	21 AAB11700	PFK-C-E-HIS fusi
4	1720	100.0	317	21 AAV93689	Human serine prote
5	1720	100.0	317	22 AAY72890	Mouse serine prote
6	1720	100.0	317	22 AAB80259	Human serine prote
7	1720	100.0	325	22 AAU23215	Novel human enzyme
8	1720	100.0	325	22 AAU17037	Human novel secret
9	1720	100.0	351	22 AAU16966	Human novel secret
10	1714	99.7	322	22 AAU23751	Novel human enzyme
11	1714	99.7	322	22 AAU17038	Human novel secret

SUMMARIES

8	Query	Match	Length	DB ID	Description
1	1720	100.0	317	20 AAV06482	Human tumour-assoc Amino acid sequenc
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8	1720	100.0	325	22 AAU17037	Human novel secret
9	1720	100.0	351	22 AAU16966	Human novel secret
10	1714	99.7	322	22 AAU23751	Novel human enzyme
11	1714	99.7	322	22 AAU17038	Human novel secret

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	99.2	319	21 AAB11701	Human serine prote
13	1626	94.5	306	21 AAB11702	Human serine prote
14	1484	86.3	327	22 AAY72891	Amino acid sequenc
15	1444	84.0	302	21 AAB11708	PFK-C-E-HIS fusi
16	1310	76.2	308	21 AAB11709	Human serine prote
17	1157	67.3	234	21 AAB11706	Mouse serine prote
18	1074	62.4	207	21 AAB11704	Human serine prote
19	1047	60.9	207	21 AAB11704	Human serine prote
20	1017	59.1	231	22 AAG7586	Human colon cancer
21	739	43.0	290	21 AAY73388	HTRM clone 3376404
22	739	43.0	290	22 AAM9388	Human polypeptide
23	739	43.0	290	22 AAU12282	Human PR04327 poly
24	739	43.0	290	22 AAEE03822	Human gene 4 encod
25	739	43.0	290	22 AAB03945	Human protease T
26	734	42.7	328	22 AAM41174	Human polypeptide
27	730	42.4	297	19 AAW77304	Amino acid sequenc
28	680	39.6	315	22 AAB13946	Fusion protein of
29	645	37.5	131	21 AAB11705	Human serine prote
30	628	36.5	284	22 AAU0467	Recombinant human
31	585	34.0	316	22 AAU04648	Human protease T
32	582	33.9	319	21 AAB16481	Fusion gene with h
33	582	33.9	319	22 AAE06934	Amino acid sequenc
34	581	33.8	328	21 AAB6480	Fusion gene with h
35	581	33.8	328	22 AAB7540	Amino acid sequenc
36	554	32.2	276	19 AAW64242	Murine mast cell p
37	554	32.2	276	19 AAW63172	Mouse mast cell p
38	549	31.9	658	22 AAE06934	Human membrane-typ
39	549	31.9	658	22 AAE06934	Human membrane-typ
40	547	31.8	802	20 AAY1710	Human PRO0618 prote
41	547	31.8	802	21 AAB4266	Human PRO0618 (UNQ3
42	547	31.8	802	21 AAB4052	Human PRO0618 prote
43	538	31.3	274	19 AAW64234	Rat homologue of m
44	536	31.2	314	19 AN7297	Amino acid sequenc
45	534	31.0	235	22 AAEE06932	Human membrane-typ

ALIGNMENTS

RESULT 1
 AAY06482 standard; Protein: 317 AA.
 ID AAY06482;
 XX AC AAY06482;
 XX DT 27-SEP-1999 (first entry)
 XX DE Human tumour-associated protein PRO343.
 XX KW PRO343; UNQ302; cancer; tumour; diagnosis; therapy; human.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Location/Qualifiers
1..32 "signal peptide"
33..317 "mature protein"
34..317 "mature protein"
35..317 "mature protein"
36..317 "mature protein"
37..317 "mature protein"
38..317 "mature protein"
39..317 "mature protein"
40..317 "mature protein"
41..317 "mature protein"
42..317 "mature protein"
43..317 "mature protein"
44..317 "mature protein"
45..317 "mature protein"

XX FN WO9935170-A2.

XX Key

FT Peptide

FT Protein

FT Modified-site

XX Location/Qualifiers

1..32 "signal peptide"

33..317 "mature protein"

99W0-US00106.

99W0-US0106.

98US-0070440.

98US-003500.

98US-006414.

98US-0098742.

98US-0107783.

XX	PA (GETH) GENENTECH INC.	KW congenital microvillus atrophy; skin disease; cell growth;
XX		KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
PI	Botsstein D, Goddard A, Gurney AL, Hillian KJ, Lawrence DA;	KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
PI	Roy MA, Wood WI;	KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
XX	DR; 1999-430385/36.	KW anti-thrombotic; wound healing; tissue repair.
DR	N-PSDB; AAX87259.	XX OS Homo sapiens.
XX	PR Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment	XX PN W09914328-A2.
PT	PT	XX XX
XX	PS Example 1; Fig 12; 162pp; English.	PD 25-MAR-1999.
XX	CC This sequence represents human PRO43 (UNQ302), a protein encoded by the novel cDNA clone DNA43318 (see AAX87259). Amplification of DNA43318 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO43 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY0647-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnostic kits.	XX XX
CC	CC	PR 16-SEP-1998; 98WO-US19330.
CC	CC	PR 25-NOV-1997; 97US-0066840.
CC	CC	PR 17-SEP-1997; 97US-0059113.
CC	CC	PR 17-SEP-1997; 97US-0059115.
CC	CC	PR 17-SEP-1997; 97US-0059117.
CC	CC	PR 17-SEP-1997; 97US-0059119.
CC	CC	PR 17-SEP-1997; 97US-0059121.
CC	CC	PR 17-SEP-1997; 97US-0059122.
CC	CC	PR 17-SEP-1997; 97US-0059184.
CC	CC	PR 18-SEP-1997; 97US-0059263.
CC	CC	PR 18-SEP-1997; 97US-0059466.
CC	CC	PR 15-OCT-1997; 97US-0062125.
CC	CC	PR 15-OCT-1997; 97US-0062285.
CC	CC	PR 17-OCT-1997; 97US-0062287.
CC	CC	PR 21-OCT-1997; 97US-0063486.
CC	CC	PR 24-OCT-1997; 97US-0062814.
CC	CC	PR 24-OCT-1997; 97US-0062816.
CC	CC	PR 24-OCT-1997; 97US-0063045.
CC	CC	PR 24-OCT-1997; 97US-0063120.
CC	CC	PR 24-OCT-1997; 97US-0063127.
CC	CC	PR 24-OCT-1997; 97US-0063128.
CC	CC	PR 27-OCT-1997; 97US-0063229.
CC	CC	PR 28-OCT-1997; 97US-0063327.
CC	CC	PR 28-OCT-1997; 97US-0063341.
CC	CC	PR 28-OCT-1997; 97US-0063542.
CC	CC	PR 28-OCT-1997; 97US-0063544.
CC	CC	PR 28-OCT-1997; 97US-0063549.
CC	CC	PR 28-OCT-1997; 97US-0063550.
CC	CC	PR 29-OCT-1997; 97US-0063364.
CC	CC	PR 29-OCT-1997; 97US-0063435.
CC	CC	PR 29-OCT-1997; 97US-0063704.
CC	CC	PR 29-OCT-1997; 97US-0063732.
CC	CC	PR 29-OCT-1997; 97US-0063738.
CC	CC	PR 29-OCT-1997; 97US-0063734.
CC	CC	PR 12-NOV-1997; 97US-0064215.
CC	CC	PR 29-OCT-1997; 97US-0063735.
CC	CC	PR 31-OCT-1997; 97US-0063870.
CC	CC	PR 18-NOV-1997; 97US-0065693.
CC	CC	PR 21-NOV-1997; 97US-0064103.
CC	CC	PR 03-NOV-1997; 97US-0063364.
CC	CC	PR 07-NOV-1997; 97US-0064809.
CC	CC	PR 12-NOV-1997; 97US-0065186.
CC	CC	PR 17-NOV-1997; 97US-0065846.
CC	CC	PR 24-NOV-1997; 97US-0066770.
CC	CC	PR 24-NOV-1997; 97US-0066511.
CC	CC	PR 24-NOV-1997; 97US-006453.
XX	AC AAY13391 standard; Protein: 317 AA.	XX PA (GETH) GENENTECH INC.
XX	DT 25-JUN-1999 (first entry)	XX PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J,
XX	DE Amino acid sequence of protein PRO43.	XX DR WPI; 1999-22533/19.
XX	KW Secreted protein; transmembrane protein; human; enterocolitis;	XX DR N-PSDB; AAX5262.
XX	KW Zollinger-Ellison syndrome; gastrointestinal ulceration;	XX PT New isolated human genes and polypeptides used in, e.g. treatment of

PT PT
XX PN WO200031277-A1.
PS XX
XX PD 02-JUN-2000.
CC XX
CC 19-NOV-1999; 99WO-JP06472.
CC XX
CC 20-NOV-1998; 98JP-0347813.
CC XX
CC PA (FUSO) FUSO PHARM IND LTD.
CC XX
CC PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
CC XX
CC DR WPI; 2000-4-00084/34.
CC XX
PT Serine protease BSSP4 and antibodies recognizing BSSP4 for assay and
PT diagnosis of diseases in which BSSP4 expression is altered
XX PS Claim 1: Page 66-67; 111pp; Japanese.
XX PS DR
XX PS Page 66-67; 111pp; Japanese.
CC The invention relates to novel serine proteases designated BSSP4
CC (AAAl695-A61704, AAAl799), and to nucleic acids encoding them (AAAl695-A61704,
CC AAAl799). The invention also relates to vectors and transformation
CC comprising BSSP4 nucleic acids; transgenic animals in which the
CC expression level of BSSP4 can be varied; and an mBSSP4 knockout mouse.
CC The invention additionally encompasses anti-BSSP4 antibodies and methods
CC of production of such antibodies, methods of BSSP4 detection using the
CC antibodies, and the use of BSSP4 proteins or fragments as diagnostic
CC markers for certain medical conditions. Nucleotides encoding BSSP4 were
CC initially isolated in a human brain cDNA library using degenerate PCR
CC primers (AAAl711-A61715) based on conserved regions of serine
CC proteases. The BSSP4 serine proteases and nucleotides encoding them are
CC useful in detecting homologues, mutants and polymorphic variants in
CC biological samples (e.g., blood, urine, brain, prostate gland and testis)
CC as diagnostic markers for diseases associated with altered BSSP4
CC expression levels. Such diseases include Alzheimer's disease, oedema
CC (cerebral), cancer or inflammation of brain, prostate, testis or bone.
CC Sequences AAAl695-A61703 and AAAl799 represent cDNAs encoding human
CC BSSP4 variants (hBSSP4), and sequence AAAl704 represents cDNA encoding
CC murine BSSP4 (mBSSP4). Sequences AAAl700-B11708 represent human BSSP4
CC variants (hBSSP4), and sequence AAAl709 represents murine BSSP4
CC (mBSSP4).
XX Sequence 317 AA;
SQ Sequence 317 AA;

Query Match 100.0%; Score 1720; DB 20; Length 317;
Best Local Similarity 100.0%; Pred. No 3.2e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 317; Conservative 0; Gaps 0;

QY 1 MVVSGAPPALGGCLGTFPSILLASTAILNAAIRIPVPPACGKFDQQLNRRVGGEDSTDSE 60
DB 1 mvvsgappalggclgtfpsiillastailnaaairipvppacgkfdqqlnrrvggedstase 60
QY 61 WPWIVSIQNGTHHAGSLLTISRVITAAHCFKDNLNRKFYFLSYVLLGAWLQGNFGSRSK 120
DB 61 wpwivsiqngthhagcslslltisrvitaahcfnlnrkyflsyvllgawlqgnfgsrsk 120
QY 61 wpyivsiqngthhagcslslltisrvitashfcfnlnrkyflsyvllgaqlqrgpsrsqk 120
DB 61 wpyivsiqngthhagcslslltisrvitashfcfnlnrkyflsyvllgaqlqrgpsrsqk 120
QY 121 VGVAVWEPHYSWKEGACADIALYRLERSIORSERVLPICLPDASILHPPNTHCWIISGW 180
DB 121 vgvawwephyswkegacadiavrlersiqservlpiclpdasihlppnthsicwiisgw 180
QY 181 GSTONGVPLPHQTLQKIKVPIIDSEVCSHUYWWGAGCPITEOMLCAGYLEGERDAIG 240
DB 181 qsiqgqvplphqtlqkikvpidsevcshuywwgaggpitedmlcgylegerdaig 240
QY 241 DSGGPLMCOVDGAWLLAGLTSGGCAERNPGYIISLSAHSRSHVEKIVQVQLRGRAG 300
DB 241 dsggpilmcovdgawllagltsggcaernpgyiislsahsrsvhvekivqvgqrlgragg 300
QY 301 GGAIRAPSOGSAARS 317
DB 301 ggaairapsogsaars 317

RESULT 3
AAB11700 Human serine protease BSSP4 (hBSSP4) SEQ ID NO:2.
AAB11700 standard; Protein: 317 AA.
XX DE Human serine protease BSSP4 (hBSSP4) first entry
XX AC DSGGPILMCOVDGAWLLAGLTSGGCAERNPGYIISLSAHSRSHVEKIVQVQLRGRAG
XX KW BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain;
XX KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
XX KW oedema; biopsy; cancer; inflammation; prostate; testis; bone.
XX OS Homo sapiens.

RESULT	4	New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation -
ID	AAY93689	standard; Protein; 317 AA
XX		
AC	AAY93689;	
XX		
DT	03-OCT-2000	(first entry)
XX		
DE	Amino acid sequence of novel polypeptide PRO343.	
XX		
KW	PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO112; PRO509; PRO853; PRO882; tumour cell; tumorigenesis; cancer; neoplastic cell growth; cell proliferation.	
KW		
KW		
OS	Homo sapiens.	
XX		
FH		
FT Peptide		Location/Qualifiers
FT	1..32	/note= "signal sequence"
FT Region	4..15	/note= "prokaryotic membrane lipoprotein attachment site"
FT Modified-site	5..11	/note= "N-myristoylation site"
FT Modified-site	12..18	/note= "N-myristoylation site"
FT Modified-site	13..19	/note= "N-myristoylation site"
FT Modified-site	16..22	/note= "N-myristoylation site"
FT Modified-site	52..58	/note= "N-myristoylation site"
FT Modified-site	70..74	/note= "N-glycosylation site"
FT Modified-site	71..77	/note= "N-myristoylation site"
FT Modified-site	77..83	/note= "N-myristoylation site"
FT Active-site	86..92	/note= "active site for serine protease"
FT Modified-site	112..118	/note= "N-myristoylation site"
FT Region	178..182	/note= "glycosylation attachment site"
FT Modified-site	273..279	/note= "N-myristoylation site"
FT Modified-site	310..316	/note= "N-myristoylation site"
XX	WO200037640-A2.	RESULT 5
PN		AAY72890
XX		ID AAY72890 standard; Protein; 317 AA.
PD	29-JUN-2000.	XX
XX		AC AAY72890;
PF	16-DEC-1999;	XX
XX	99WO-US30095.	DT 31-MAY-2001 (first entry)
PR	22-DEC-1998;	XX
PR	08-MAR-1999;	DE Human serine protease, protease C-E.
PR	02-JUN-1999;	XX
PR	01-SEP-1999;	KW Human; serine protease; protease C-E; therapy; desquamation; skin care; laundry detergent; shampoo; cleaning agent; hair care; skin flaking; neurodegenerative disorder; dermatological; immunogenic; proteolytic.
PR	15-SEP-1999;	KW
PR	30-NOV-1999;	KW
PR	30-NOV-1999;	KW
PR	01-DEC-1999;	KW
PR	02-DEC-1999;	KW
XX	PA (GETH) GENENTECH INC.	chromosome 16p13.3.
XX	Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;	XX
PI	Wood WI;	OS Homo sapiens.
XX		XX
DR	WPI: 2000-452188/39.	PN WO200116288-A2.
DR	N-FSDB; AAA46914.	PD 08-MAR-2001.
DR		XX
PR	31-AUG-1999;	PF 14-AUG-2000; 2000WO-US22117.
PR		XX
PR		PR 31-AUG-1999; 99US-0386629.

Db	121	vgavawephpswkegacadiavrlersiqfserpicldashlppnthsicwgw	180		PR	22-AUG-2000;	20000US-0226868.
QY	181	GSIQGVPFLPHQTLPLQLKVPITIDEVCVSHLYNGAGCOPITEMLCAGYLEGERDACLG	240		PR	22-AUG-2000;	20000US-0221182.
Db	181	gsiqgvpflphqtlplqlkvpitidevcvshlyngagcopicldmlcagylegerdaci	240		PR	23-AUG-2000;	20000US-0227009.
QY	241	DGGPBLMCQVDGMLLAGLISWGGCAERNPGVYISLSAHRSHVEKIVQGVLRGAG	300		PR	30-AUG-2000;	20000US-0228924.
Db	241	dsggpblmcqvdgmllagliswggcaernpgvysisahrswekiivqgvlrgrqq	300		PR	01-SEP-2000;	20000US-0229387.
QY	301	GGAIRAPSQSGAAARS	317		PR	01-SEP-2000;	20000US-0229343.
Db	301	ggairapsqsgaaars	317		PR	01-SEP-2000;	20000US-0229344.
RESULT	7				PR	05-SEP-2000;	20000US-0229309.
AAU2215					PR	05-SEP-2000;	20000US-0229313.
ID	AAU2215	standard; Protein; 325 AA.			PR	06-SEP-2000;	20000US-0230437.
XX					PR	06-SEP-2000;	20000US-0230438.
AC	AAU2215;				PR	08-SEP-2000;	20000US-0231242.
XX					PR	08-SEP-2000;	20000US-0231244.
DT	17-DEC-2001	(first entry)			PR	08-SEP-2000;	20000US-0231413.
XX					PR	08-SEP-2000;	20000US-0231414.
DE	Novel. human enzyme polypeptide #301.				PR	08-SEP-2000;	20000US-0232080.
XX					PR	08-SEP-2000;	20000US-0233081.
AC	AAU2215;				PR	12-SEP-2000;	20000US-0231968.
XX					PR	12-SEP-2000;	20000US-0232397.
KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;				PR	14-SEP-2000;	20000US-0233398.
KW	ligase; hyperproliferative disorder; immunodeficiency disorder;				PR	14-SEP-2000;	20000US-0234299.
KW	autoimmune disorder; neurological disorder; metabolic disorder;				PR	14-SEP-2000;	20000US-0234240.
KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;				PR	14-SEP-2000;	20000US-0233406.
KW	blood-related disorder; infectious disorder; cytosstatic; anti arthritic;				PR	14-SEP-2000;	20000US-0233065.
KW	nephrotropic; anticoagulant.				PR	14-SEP-2000;	20000US-0234998.
XX					PR	14-SEP-2000;	20000US-0235064.
OS	Homo sapiens.				PR	14-SEP-2000;	20000US-0234997.
XX					PR	14-SEP-2000;	20000US-0234997.
PN	W0200155301-A2.				PR	14-SEP-2000;	20000US-0235337.
XX					PR	14-SEP-2000;	20000US-0235337.
PD	02-AUG-2001.				PR	14-SEP-2000;	20000US-0235367.
XX					PR	14-SEP-2000;	20000US-0235367.
PF	17-JAN-2001; 2001IW0-US01239.				PR	14-SEP-2000;	20000US-0235368.
XX					PR	14-SEP-2000;	20000US-0235368.
PR	31-JAN-2000; 20000US-0179065.				PR	14-SEP-2000;	20000US-0235369.
PR	04-FEB-2000; 20000US-0180628.				PR	14-SEP-2000;	20000US-0235370.
PR	24-FEB-2000; 20000US-0184664.				PR	14-SEP-2000;	20000US-0235370.
PR	02-MAR-2000; 20000US-0186150.				PR	14-SEP-2000;	20000US-0235370.
PR	16-MAR-2000; 20000US-0188974.				PR	14-SEP-2000;	20000US-0235370.
PR	17-MAR-2000; 20000US-0190076.				PR	14-SEP-2000;	20000US-0235370.
PR	18-APR-2000; 20000US-0198123.				PR	14-SEP-2000;	20000US-0235370.
PR	19-MAY-2000; 20000US-0205151.				PR	14-SEP-2000;	20000US-0235370.
PR	07-JUN-2000; 20000US-0209467.				PR	14-SEP-2000;	20000US-0235370.
PR	28-JUN-2000; 20000US-0214866.				PR	14-SEP-2000;	20000US-0235370.
PR	30-JUL-2000; 20000US-021135.				PR	14-SEP-2000;	20000US-0235370.
PR	07-JUL-2000; 20000US-021647.				PR	14-SEP-2000;	20000US-0235370.
PR	07-JUL-2000; 20000US-021680.				PR	14-SEP-2000;	20000US-0235370.
PR	11-JUL-2000; 20000US-0217487.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0217496.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-021890.				PR	14-SEP-2000;	20000US-0235370.
PR	26-JUL-2000; 20000US-0220963.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0220964.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0224518.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0224519.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225213.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225214.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225266.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225267.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225268.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225269.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225270.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225447.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225577.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225758.				PR	14-SEP-2000;	20000US-0235370.
PR	14-AUG-2000; 20000US-0225759.				PR	14-SEP-2000;	20000US-0235370.
PR	18-AUG-2000; 20000US-0226279.				PR	14-SEP-2000;	20000US-0235370.
PR	22-AUG-2000; 20000US-0226681.				PR	14-SEP-2000;	20000US-0235370.
					PR	17-Nov-2000;	20000US-0249207.

PR	17-NOV-2000; 2000US-0249208.	QY	1 MIVSGAPPALGGGCLGLTFTSLILLASTAILNAAIRIPVPPACGKPKQQLNRYVGGEDSTDE 60
PR	17-NOV-2000; 2000US-0249209.	Db	9 mvvsgappaiggggltttslllastailnaairipvppacgkpkqqlnryvggedstde 68
PR	17-NOV-2000; 2000US-0249210.	QY	61 WPMIVSICKNGTHHCAGSLLTSRNVITAHHCFKDNLNKPYLFSVYLGAWLGNPGSRGOK 120
PR	17-NOV-2000; 2000US-0249211.	Db	69 wpivsickngthhcagslltsrwitaahcfkdnlnkpylfsvylqwglnpgsrqk 128
PR	17-NOV-2000; 2000US-0249212.	QY	121 VGYAWVEPHPVYSIKEGACADIALVRLERSIQSERVLPICLDPASILPPNTHCWISGW 180
PR	17-NOV-2000; 2000US-0249213.	Db	129 vgyawvephpvysmkegacadiavrlrsiqservlpicldpasilppnthcwsgw 188
PR	17-NOV-2000; 2000US-0249214.	QY	181 GSIQDGVPILPHPOTPLQKLKVPIIDSECVSHLYWNRGAGGSPITEDMLCAGYLEGERDAGLG 240
PR	17-NOV-2000; 2000US-0249215.	Db	189 gsiqdgvplphpotplqklkvpidsecvshlywrgaggspitedmlcagylegerdalg 248
PR	17-NOV-2000; 2000US-0249217.	QY	241 DSGGPILMCOVDGAWLLAGTISWEGGCAERNRPGVYIISLSAHRSWKEVKYQGVOLRGRQG 300
PR	17-NOV-2000; 2000US-0249218.	Db	249 dsggpilmcovdgawllagiswsgcaernrpavyislsahrswevkvqgvqlrqraqq 308
PR	05-DEC-2000; 2000US-0249244.	QY	301 GGALARPSQSGGAAARS 317
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PR	17-NOV-2000; 2000US-0249297.	XX	standard; Protein; 325 AA.
PR	17-NOV-2000; 2000US-0249299.	AAU17037;	
PR	01-DEC-2000; 2000US-0249300.	AC	
PR	01-DEC-2000; 2000US-0250160.	XX	
PR	01-DEC-2000; 2000US-0250391.	DT	07-NOV-2001 (first entry)
PR	05-DEC-2000; 2000US-0251030.	XX	
PR	05-DEC-2000; 2000US-0251988.	DE	Human novel secreted protein, SEQ ID 278.
PR	05-DEC-2000; 2000US-0256719.	XX	
PR	06-DEC-2000; 2000US-0251479.	KW	Human; immunosuppressive; antiarthritic; antirheumatic;
PR	08-DEC-2000; 2000US-0251856.	KW	cystostatic; cardiotropic; vasotropics; cerebroprotective; nootropic;
PR	08-DEC-2000; 2000US-0251868.	KW	neuroprotective; antibiotic; antiviral; fungicide; opthalmological;
PR	08-DEC-2000; 2000US-0251989.	KW	vulnery; secreted protein; rheumatoid arthritis;
PR	08-DEC-2000; 2000US-0251990.	KW	hypoproliferative disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis;
PR	11-DEC-2000; 2000US-0254097.	KW	nervous system disorder; Alzheimer's disease; infection; ocular disorder;
PR	05-JAN-2001; 2001US-0259678.	KW	corneal infection; wound healing; epithelial cell proliferation;
XX		KW	skin ageing; food additive; preservative; antiproliferative.
PA (HUMA -) HUMAN GENOME SCI INC.		XX	
PA		XX	Homo sapiens.
PAI	Rosen CA, Barash SC, Ruben SM;	XX	
XX		XX	
DR	WPI; 2001-465566/50.	PN	WO200155441-A2.
DR	N-PDB; AAS41085.	XX	
XX		XX	
PT	Novel polypeptides and poly nucleotides useful for diagnosing,	PD	02-AUG-2001.
PT	preventing, treating neural, immune system, muscular, reproductive,	XX	
PT	pulmonary, cardiovascular, renal, proliferative disorders and cancerous	XX	
PT	diseases	XX	
XX		XX	
CC	Claim 11; SEQ ID No 1211; 1180PP; English.	XX	
CC	The present invention relates to the isolation of novel human enzyme	XX	
CC	polypeptides, and the cDNA and genomic sequences	XX	
CC	encoding them. The enzyme polypeptides of the invention may comprise the	XX	
CC	functional classes of oxidoreductases, transferases, hydrolases, lyases,	XX	
CC	isomerases or ligases. The sequences of the invention are useful in the	XX	
CC	diagnosis, treatment and/or prognosis of a wide range of	XX	
CC	disorders including hyperproliferative disorders (e.g. cancer),	XX	
CC	immuno deficiency disorders (e.g. AIDS) autoimmune disorders	PR	31-JAN-2000; 2000US-0179065.
CC	(e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),	PR	04-FEB-2000; 2000US-0180628.
CC	metabolic disorders (e.g. phenylketonuria), inflammatory disorders	PR	24-FEB-2000; 2000US-0184664.
CC	(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),	PR	02-MAR-2000; 2000US-0186350.
CC	blood related disorders (e.g. haemophilia), reproductive disorders	PR	16-MAR-2000; 2000US-0190874.
CC	(e.g. infertility) and infectious disorders (e.g. Influenza). The	PR	17-MAR-2000; 2000US-019076.
CC	polynucleotides of the invention can also be used in gene therapy.	PR	18-APR-2000; 2000US-0188123.
CC	AAU22915 AAU23814 represent the novel human enzyme polypeptides of the	PR	19-MAY-2000; 2000US-0205515.
CC	invention.	PR	07-JUN-2000; 2000US-0209467.
CC	Note: The sequence data for this patent did not form part of the printed	PR	28-JUN-2000; 2000US-0214886.
CC	specification, but was obtained in electronic format directly from WIPO	PR	30-JUN-2000; 2000US-0215135.
CC	at ftp.wipo.int/pub/published_pct_sequences.	PR	07-JUL-2000; 2000US-0216647.
XX		PR	07-JUL-2000; 2000US-0216880.
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SQ		PR	11-JUL-2000; 2000US-0217496.
PR	Query Match 100.0%; Score 1720; DB 22; Length 325;	PR	26-JUL-2000; 2000US-0220963.
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SQ		PR	14-AUG-2000; 2000US-0224519.

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PR	14 - AUG -2000;	2000US-0225214.
PR	14 - AUG -2000;	2000US-0225216.
PR	14 - AUG -2000;	2000US-0225267.
PR	14 - AUG -2000;	2000US-0225268.
PR	14 - AUG -2000;	2000US-0225447.
PR	14 - AUG -2000;	2000US-0225757.
PR	14 - AUG -2000;	2000US-0227182.
PR	14 - AUG -2000;	2000US-0227009.
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PR	22 - AUG -2000;	2000US-0227182.
PR	23 - AUG -2000;	2000US-0228924.
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PR	01 - SEP -2000;	2000US-0229344.
PR	01 - SEP -2000;	2000US-0229345.
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PR	06 - SEP -2000;	2000US-0230431.
PR	06 - SEP -2000;	2000US-0231048.
PR	08 - SEP -2000;	2000US-0231242.
PR	08 - SEP -2000;	2000US-0231243.
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PR	08 - SEP -2000;	2000US-0232401.
PR	12 - SEP -2000;	2000US-0231198.
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PR	02 - OCT -2000;	2000US-0236802.
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PR	02 - OCT -2000;	2000US-0237038.
PR	02 - OCT -2000;	2000US-0237039.
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PR	08 - NOV -2000;	2000US-0246475.
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PR	08 - NOV -2000;	2000US-0246477.

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11 -DEC-2000; 2000US-0254097-
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05 -JAN-2001; 2001US-0259678-
XX
(HUMA-) HUMAN GENOME SCI INC
Rosen CA, Barash SC, Ruben
WPI: 2001-476222/51.
N-PSDB; AAS6942.

Claim 11; SEO ID NO 278; 601PP; English

Temporary benthic index of habitat quality

disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to unburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
Query Match Score 100.0%; Score 1720; DB 22; Length 325;
Best Local Similarity 100.0%; Prid. No. 3.3e-147; 0; Indels 0; Gaps Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps
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Qy 121 VGVAVVEPHPVYSWKEGACADIALYRLERSIQFSERVLPCLPDASIHLPPTNTHCMISGW 180 Db 129 vgvavvephpvyswkegacadiayrlersiqfservlpclpdsishlpptnths 188
Qy 181 GSIDQGPVLPHPTQIQLKVPITIDSEVCSHLYWRGAGQPTIEDMICAGTLEGERDACLG 240 Db 189 gsidqgpvlphptqikvpitdsevcshlywrqaggqptiedmicagtylegerdac 248
Qy 241 DSGGPITMCQVDGAWNLJAGITSWGECAERNRPQGYTISLSAHRSWYEKIVQYQLGRAQG 300 Db 249 dsggpitmcqvdgawnljagitswgecaernrpqgytislsahrswyequivqyqlgrraqg 308
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RESULT 9 AAU16966 ID AAU16966 standard; Protein: 351 AA. XX AC AAU16966; XX DT 07-NOV-2001 (first entry) XX DE Human novel secreted protein, SEQ ID 207. XX KW Human; immunosuppressive; antiarthritic; antirheumatic; KW cytostatic; cardiot; vasotrop; cerebroprotective; nootropic; KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological; KW vulnerability; secreted protein; rheumatoid arthriti; KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest; KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; KW nervous system disorder; Alzheimer's disease; infection; ocular disorder; KW corneal infection; wound healing; epithelial cell proliferation; KW skin ageing; food additive; preservative; antiproliferative. XX OS Homo sapiens. XX PN WO200155441-A2. XX PD 02-AUG-2001. XX PF 17-JAN-2001; 2001WO-US01320. XX PR 31-JAN-2000; 2000US-0179065. PR 04-FEB-2000; 2000US-0180638. PR 24-FEB-2000; 2000US-0184664. PR 02-MAR-2000; 2000US-0186350. PR 16-MAR-2000; 2000US-018874. PR 17-MAR-2000; 2000US-0190076. PR 17-APR-2000; 2000US-0198123.

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PR	14-SEP-2000;	20000TS-0233013.	PR 08-DEC-2000; 20000US-0251868.
PR	14-SEP-2000;	20000TS-0233014.	PR 08-DEC-2000; 20000US-0251169.
PR	21-SEP-2000;	20000TS-0233015.	PR 05-DEC-2000; 20000US-0251989.
PR	21-SEP-2000;	20000TS-0234040.	PR 08-DEC-2000; 20000US-0251990.
PR	25-SEP-2000;	20000TS-0234041.	PR 11-DEC-2000; 20000US-0254097.
PR	25-SEP-2000;	20000TS-0234042.	PR 05-JAN-2001; 2001US-0259678.
PR	26-SEP-2000;	20000TS-0235498.	XX PA (HUNA-) HUMAN GENOME SCI INC.
PR	27-SEP-2000;	20000TS-0235834.	XX PI Rosen CA, Barash SC, Ruben SM;
PR	27-SEP-2000;	20000TS-0235836.	XX DR WPI: 2001-465566/50.
PR	29-SEP-2000;	20000TS-0235367.	DR N-PSDB; AAS41621.
PR	29-SEP-2000;	20000TS-0236368.	DR

XX Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases -

XX Claim 11; SEQ ID NO 1747; 118QPP; English.

CC The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AS40785-AS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.

CC AAU2015-AAU23814 represent the novel human enzyme polypeptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fp.wipo.int/pdb/published_pct_sequences.

XX Sequence 322 AA;

Query Match 99.7%; Score 1714; DB 22; Length 322;
Best Local Similarity 99.7%; pred. No. 1.1e-146; Indels 0; Gaps 0;

Matches 316; Conservative 0; Mismatches 1; Gaps 0;

Qy	1	MVSGAPPALGGCCIGTFTSILLASTAINAARIYPVPPACGKPDQLNRVVGGEDSTDSE	60
Db	6	mvsgappalggccigtftsillastainaaariypvppacgkpdqlnrvggedstase	65
Qy	61	WPWISIQKNGTHAGSLTSRWITAAHCFKDNLNKPLFSVLGAQQLGNPGRSOK	120
Db	66	wpwisyxkgthcags11tsrwitaahfckhnlnkylfsvlqawqlqngdgsrsk	125
Qy	121	VGVANVEPHVYSNKEGACADIALYRLERSIQSERVILPCLPDASILHPNTHCWISGW	180
Db	126	vgvawvephvyswiegacadiavrlersiqservilcpdasilhpnnthcwisgw	185
Qy	181	GSIQDGVPILPHPTOLQKLWPKIIDSEVCSHLWYRAGGQPITEDMLCAGYLEGERDACLG	240
Db	186	gsiqdgvpilphptolqklwpkildsevcshlywraggqpitedmlcagylegerdaclg	245
Qy	241	DSGGPILMCQVDGAWLGIISWGECAERNRPGYIISLAHSRVEKIVQGVQLRGAG	300
Db	246	dsggpilmcqvdgawlagiswgecaernrpgyiislahsrvekivqgvqlrgagg	305
Qy	301	GGALARPSQSGAAARS 317	
Db	306	ggalarpsqsgaaars 322	

RESULT 11
ID AAU17038
XX AAU17038 standard; Protein; 322 AA.
XX DT 07-Nov-2001 (first entry)
XX Human novel secreted protein, SEQ ID 279.
DE XX
KW XX Human; immunosuppressive; antiarthritic; antirheumatic;
KW cytotoxic; cardiotonic; vasotropics; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmological;

CC murine BSSP4 (mBSSP4). Sequences AAB11700-B11708 represent human BSSP4 variants (hBSSP4), and sequence AAB11709 represents murine BSSP4 (mBSSP4).

XX Sequence 306 AA;

Query Match 94.5%; Score 1626; DB 21; Length 306;
Best Local Similarity 97.4%; Pred. No. 9.5e-139; 1; Mismatches 1; Indels 6; Gaps 1;

XX WO9836054-A1.

QY 1 MIVVSGAPPALGGCGLGTFNSLILLASTAILNARARIPIPVPAPACGPQQLARVGGEDSTDSE 60
DB 1 mivvsgappalggcglgtfctsllastailnaraipiypacgpqqlarvyygedstdse 60

XX 20-AUG-1998.
PR 13-FEB-1998; 98WO-AU00085.

QY 61 WPWIVS1QNGTHICAGSLTSRWNVTAHCFKDNLNPKYLFSVLLGWOLGNGPSRSQK 120
DB 61 wpwivs1qngthicagsltsrwitahcfkdnlnpkylfsv1lgawqlgpgsrsqk 120

XX 18-NOV-1997; 97AU-0000422.
PR 13-FEB-1997; 97AU-0005101.

QY 121 VGYAWVEPHPVYSWKEGACADIALVRERSIQFSERVLPICLPDASTHLPNTHCWISGW 180
DB 121 vgyawvephpvyswkegacadiavrlersiqfservlpiclpdasthlpnhtcwisgw 180

XX PA (AMRA) AMRAD OPERATIONS PTY LTD.

QY 181 GSTIDGVPPLPHPQTLQKLKVPIIDSEVCSSHLYWRGAGGQPITEDMLCAGYLEGERDACL 240
DB 181 gsdidgvpplphpqtliqklkvpidsevcshlywrqaggqpitedmlcagylegerdaci 240

XX DR 1998-480768/41.
DR-N-PSDB; AAV59134.

QY 241 DSGGPMQCDGAVLLAGLISWGSGCAEENRPGVYISLSAHSRSWEKLVQGVQLRGRAQ 300
DB 241 dsggpmcqcdgavllagliswgsgcaenrpgvysisahsrswekivqgvqrlgrpr-- 298

XX PS Example 15; Fig 20A; 167PP; English.

QY 301 GAIURAPS 308
DB 299 ---rapa 302

XX XX AAW7302-04 represent HELA2 homologues. The genes are found in a cluster on chromosome 16p13.3. HELA2 was isolated from HeLa cells, and has homology to serine proteases. The protein is involved in or associated with regulation of cell activity and/or viability. Administration of recombinant HELA2 (also called testisin) is used to increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is also a suppressor of testicular germ cell cancers (seminoma) and is also expressed in some non-testicular cancers (of colon, pancreas, prostate and ovary), so is a marker/potential therapeutic target for cancer. The promoter from the HELA2 gene is useful for testis-specific expression of other genes, e.g. for gene therapy or modulation of fertility. Drugs that block activity of HELA2 should have antitumour activity (other than in testis) while in testis recombinant HELA2 should stop growth of tumours and normalise sperm development (eliminating the need for orchidectomy). Identification of mutant forms of HELA2 can be used to diagnose infertility.

XX Sequence 271 AA;

QY 86.3%; Score 1484; DB 19; Length 271;
Best Local Similarity 100.0%; Pred. No. 5.5e-126;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 LNRIVGGEDSTDSENPWIVSIQKNGTHICAGSLTSRWNVTAHCFKDNLNPKYLFSVLL 106
DB 1 Inrvgggedstdsepwivsiqkgthicagsltsrwitahcfkdnlnpkylfsvll 60

QY 107 GAWQLGNPGRSRSQKVGVAVEPHPVYSWKGACADIALVRERSIQFSERVLPICLPDAS 166
DB 61 gawqlgnpsrsqkvgvavrepvhyswkegacadiavrlersiqfservlpiclpdas 120

QY 167 IHLPPNTHCWISGMGSIDQGVPPLPHPQTLQKLKVPIIDSEVCSSHLYWRGAGGQPITEDML 226
DB 121 ihlpnthsicws1qngthicagsltsrwitahcfkdnlnpkylfsvll 180

QY 227 CAGYLEGERDACLGDGGPLMCQVDGAWLJAGLISWGEGFAERNRPGVYISLSAHSRSWE 286
DB 181 cagy-legerdaci1gsgp1mcqvdegawllagiswggecaernrpgvysisahsrswe 240

QY 287 KIVQGVQLRGRAGQGGALRAPSGQSAAARS 317

OS Homo sapiens.

XX Key Location/Qualifiers

FH Disulfide-bond 29

FT Misc-difference 44 /note= "likely to be involved in disulphide bonding"

FT Disulfide-bond 45 /note= "likely to be a catalytic residue"

FT Misc-difference 95 /note= "likely to be involved in disulphide bonding"

FT Disulfide-bond 115 /note= "likely to be a catalytic residue"

FT Disulfide-bond 129 /note= "likely to be involved in disulphide bonding"

FT Misc-difference 160 /note= "likely to be involved in disulphide bonding"

FT Disulfide-bond 162 /note= "likely to be involved in disulphide bonding"

FT Disulfide-bond 181 /note= "likely to be involved in disulphide bonding"

FT Disulfide-bond /note= "encoded by GAA"

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Result No.	Score	Match	Length	DB ID	Description
1	581.5	33.8	299	4	US-08-944-83-66
2	554	32.2	276	2	US-09-016-366A-15
3	554	32.2	276	2	US-08-978-404B-21
4	53.8	31.3	274	2	US-08-978-404B-5
5	53.1	30.9	314	4	US-09-008-71A-3
6	53.0	30.8	308	21	US-09-016-366A-21
7	53.0	30.8	274	2	US-08-978-404B-16
8	53.0	30.8	275	2	US-09-016-366A-17
9	53.0	30.8	275	2	US-08-978-404B-12
10	529.5	30.8	273	2	US-09-016-366A-19
11	529.5	30.8	273	2	US-08-978-404B-14
12	522	30.3	270	2	US-08-978-404B-8
13	519.5	30.2	273	2	US-08-978-404B-6
14	518	30.1	273	2	US-08-978-404B-3
15	514.5	29.9	267	2	US-09-016-366A-23
16	514.5	29.9	267	2	US-08-978-404B-18
17	511.5	29.7	245	4	US-08-944-483-69
18	511.5	29.7	249	4	US-09-079-970A-5
19	508	29.5	304	4	US-09-088-651-2
20	506.5	29.4	245	4	US-09-079-404B-6
21	473.5	27.5	248	4	US-08-944-483-63
22	470.5	27.4	238	4	US-08-944-483-64
23	469.5	27.3	638	2	US-08-681-151-3
24	468.5	27.2	435	4	US-09-008-271A-6
25	466	27.1	454	4	US-09-518-046-2
26	463	26.9	416	2	US-09-000-846-2
27	462	26.9	492	4	US-09-342-749-2

MOLECULE TYPE: No. 6232456e
US-08-944-483-66

US-09-016-366A-15

Query Match 33.8%; Score 581.5; DB 4; Length 299;
Best Local Similarity 45.4%; Pred. No. 6.5e-50;
Matches 113; Conservative 42; Mismatches 89; Indels 5; Gaps 4;

Qy 50 VVGGEDSTPSEWPNTIVSNGTHCAGSLTSRWTAAHCFKDNLNKPYLFSVLUGAW 109
Db 1 ITGESSAVAGQWPKVSITYEGVIVCGSLVSEOWLSSAHCPSSEHIKE-AVEVKLGKAH 59

Qy 110 QLGNPGSRSSOKVGYAWVEPPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASTHL 169
Db 60 QLDYSEDARVSTURKIDTIPSY-LQEKGQDIALLQLSPRTFSRYTRPICLPAANASF 118

Qy 170 PPNTHCWISWGSGTQDGVLPHPTOLKVKPVIDSEVCSHLYWRGA-GQGP - ITEDML 226
Db 119 PNGLHCTVWGHWYAPSVLTPKPLQQEVLPLISRETCNCNLNIDAKPEEPFHVQEDMV 178

Qy 227 CAGYLEGERDACLGDSGGPLMCQVDGAWLLAGITISWGESCACERNRGVYTISLAHRSWVE 286

Db 179 CAGYVEGGDRACQGDGGPLSCPVEGLNWLTTGIVSWGDACGARNRPGVYTASSYASIQ 238

Qy 287 KIVGQYOLR 295
Db 239 SKVTELQPR 247

RESULT 2

US-09-016-366A-15
; Sequence 15, Application US/09016366A
; Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PastSEO for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/16366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Pluner, Elizabeth R.

REGISTRATION NUMBER: B0801/7090

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 32.2%; Score 554; DB 2; Length 276;
Best Local Similarity 41.6%; Pred. No. 3.2e-47;
Matches 116; Conservative 48; Mismatches 93; Indels 22; Gaps 9;

Qy 21 LLLIATLINAARIPIPVP - PACGKRPQQLNSRNVGGEDSTOEWPMVSIQ -- -KNGTHHCA 76
Db 6 LLLIWAELLASLYVSAAPRA --- NQRVTVGHEAESSKWPQVSLRFKLKNWVHFCC 61

Qy 77 GSULTSRWVITAACFCKDNLNKPYLFSYLLGANOL - GNPGSRSSQKVGYAWVEPHPVYSSW 134
Db 62 GSLIHPQWVLTAAHCVGPHIKSPOLFRYLOREQVLYGD----QLSLNRIVVPHHYT 116

Qy 135 KEGACADIALVRLERSIQFSERVLPICLPDASTHLPPOT 194
Db 117 AEGG-ADVALLEEVPAVNVSTHTHISLPPSETFPGTGSCWVIGWDIDNDEFLPPYP 175

Qy 195 LQLKVPIDSEVCSHLVYRGAGG -- -PITED-MLCAGYLEGERDACLUDSGSPLMCOV 250
Db 176 LKQVKVPTIVENSLDKRYHTGLTYGDDFTVHDGMLCAG -- -NTRDSCQGDSSGPLVCKV 233

Qy 251 DGAWILLAGITISWGEGCAERNRGVYTISLAHRSWVEKV 289
Db 234 KGTMWQAGTVWSWGECAQPNKPGIYTTRYVYLDWIRYV 272

RESULT 3

US-08-978-404B-21
; Sequence 21, Application US/08978404B
; Patent No. 5967732
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; FIBRINogen
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pluner, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-978-404B-21

Query Match 32.2%; Score 554; DB 2; Length 276;
 Best Local Similarity 41.6%; Pred. No. 3.2e-47;
 Matches 116; Conservative 48; Mismatches 93; Indels 22; Gaps 9;

21 LLLASTALNAAARIPIVPP-PACGKPKQOLNRVGGEDSTDSEMPATIVS0---KNGTHHCA 76
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 6 LLILWALSLLAISLYSSAPRA ---NQRVGIVGHEASESKWPKQVSURFLKNYWIHFEG 61
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 77 LTLSLTSRWTTAACFKDNKPKTFLSYLGANOLP : | : | : | : | : | : | : | : |
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 62 GSЛИHPQWVLTAAHCVGPHIKSPOLFVQLREQLYYGD---QILSLNRIVHHPHYT 116
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 135 KEGACADIALYRLERSIOPSERVLPICLFDASIAHLPPNTCHCNISGMGSQDGYPLPHPT 194
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 117 AEGG ADVALLELEPVNVNSTHPIPSLPESETFPPTGTSWLTGWGDDNDDEFLPPIPP 175
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 195 LQKLKVPIIDSECVSHLYWRGAGQ---PITED-MLCAGYLEGERDACLGDSGGPLMCQV 250
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 176 LQKQVPTVENSLSLDRKTHTGTLYGDDDFIVHDGMLCAG--NTRRDSQCGDSCGPPLYCKV 233
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 251 DGAWLLAGLISWGCGCAERNPGYIISLAHRSSVEKIV 289
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 234 KGTLWLNQAGVVSWGEGCAQPNKPGIYTRVTVYLDWIHRYV 272
 1111 : :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 4
 US-08-978-404B-5
 Sequence 5, Application US/08978404B
 Patent No. 5968782

GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 TITLE OF INVENTION: FIBRINogen
 NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

COMPUTER SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,404B
 FILING DATE: 25-NOV-97
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,354
 FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 274 amino acids
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: No. 5968782

US-08-978-404B-5
 Sequence 3, Application US/09008271A
 Patent No. 6203979

GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 Yue, Henry
 Guegler, Karl J.
 Corley, Neil C.
 Tang, Tom Y.
 Shah, Parvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
 NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/008,271A
 FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Mohan-Peterson, Sheela
 REGISTRATION NUMBER: 41,201
 REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 314 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSTOT03
 CLONE: 789327

SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

us-09-008-271a-3

; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-016-366A-21

RESULT 6
; Sequence 21, Application US/09016366A
; Patent No. 595411
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Hung, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELEPHONE: 617-720-3500
; TELEX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TOPOLGY: linear
; MOLECULE TYPE: No. 5968782e

RESULT 7
; Sequence 16, Application US/08978404B
; Patent No. 5968712
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOLIN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLGY: linear
; MOLECULE TYPE: No. 5968782e

US-08-978-404B-16

Query Match 30.8%; Score 50.5; DB 2; Length 274;
 Best Local Similarity 39.28%; Pred. No. 6.8e-45;
 Matches 113; Conservative 53; Mismatches 85; Indels 37; Gaps 9;

Qy 20 SILLASTAILNARIAPIVPPACGKPKQQLNRVYGGEDSTDSEMPWIVSIQKNG---THHCA 76
 Db 2 NLLJLALPVL--ASRAYAAPAPQALORVIGTGGQEAPRSKWPWQSLRVHPYWMMHFCG 59

Qy 77 GSILTSRMRVITAHC---FKD----NLNPYLFISVLLGAWLGNPGSRQKVGYAW 126
 Db 60 GSILJHPQWVLTAAHCYGVDPDKLAALRVLRLQHLY-----YQQQLLPVSR 106

Qy 127 EPHP-VYSWKEGACADIALVRERSIQSERVLPICLDASDHLPNTCHWSGWGSID 185
 Db 107 IVHPQFYLIQTG--ADALLELEFEPVNNTSSRVHTVMLPBASETEPPGMPCWTVGDVDN 165

Qy 186 GYLPHPHPTOLQKURVPIDSEYCSHLWYRGAGQP---ITEDMLCAGLEGRDAGCD 241
 Db 165 DELLPPPPLQKVKPVIMENHICDAKYLHGAYTGDDYFLIRDMLCAG--NSORDSCKGD 223

Qy 242 SGGPLMCOYDGAVLLAGLISWEGGCAERNRPGVYIISLSAHRSMVEKTY 289
 Db 223 SGGLPLVKYNTQAGVVSWESEGCAQENRPGIYTRVYIYLWMIHYV 271

RESULT 8

US-09-016-366A-17

; Sequence 17, Application US/09016366A
 ; Patent No. 5955531

; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; INVENTION: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016_366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:

; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-09-016-366A-17

Query Match 30.8%; Score 530.5; DB 2; Length 275;
 Best Local Similarity 39.6%; Pred. No. 6.8e-45;
 Matches 114; Conservative 50; Mismatches 87; Indels 37; Gaps 9;

Qy 20 SILLASTAILNARIAPIVPPACGKPKQQLNRVYGGEDSTDSEMPWIVSIQ---KNGTHCA 76
 Db 3 SILLALALPVL--ASRAYAAPAPQALOQAGIVGQEARSRSKWNQSVTSRVRDRYWMHFCG 60

Qy 77 GSILTSRMRVITAHC---KD----NLNPYLFISVLLGAWLGNPGSRQKVGYAW 126
 Db 61 GSILJHPQWVLTAAHCYGVDPDKLAALRVLRLQHLY-----YQDOLLPVSR 107

Qy 127 EPHP-VYSWKEGACADIALVRERSIQSERVLPICLDASDHLPNTCHWSGWGSID 185
 Db 108 IVHPQFYLIQTG--ADALLELEFEPVNNTSSRVHTVMLPBASETEPPGMPCWTVGDVDN 165

Qy 186 GYLPHPHPTOLQKURVPIDSEYCSHLWYRGAGQP---ITEDMLCAGLEGRDAGCD 241
 Db 166 DELLPPPPLQKVKPVIMENHICDAKYLHGAYTGDDYFLIRDMLCAG--NSORDSCKGD 223

Qy 242 SGGPLMCOYDGAVLLAGLISWEGGCAERNRPGVYIISLSAHRSMVEKTY 289
 Db 224 SGGLPLVKYNTQAGVVSWESEGCAQENRPGIYTRVYIYLWMIHYV 271

RESULT 9

US-08-978-404B-12

; Sequence 12, Application US/08978404B
 ; Patent No. 5968782

; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; FIBRINogen
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,355
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-2441
 ; TELEFAX: 617-720-3500
 ; TELEX:

; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-978-404B-12

Query Match 30.8%; Score 530.5; DB 2; Length 275;
 Best Local Similarity 39.6%; Pred. No. 6.8e-45;
 Matches 114; Conservative 50; Mismatches 87; Indels 37; Gaps 9;

Qy 20 SILLASTAILNAAARIPIPACGPQQLNRRVGGEDSTDSEWPIVSTQ--KNGTHHCA 76
 Db 3 SLLLALPVL--ASRAYAAPVPAQQAGTIVGQEAPRSKWPQVSLSRVRDRYWMHFCG 60
 Qy 77 GSLLTSRWTAACF---KD----NLNKPYLFSVLLGAQGNPGRSRQKVGYAW 126
 Db 61 GSLLHPQWLTAAHCFLATLPDKLTLATLRVQLEQHLY--YQDQJLPVSR 105
 Qy 127 EPHP-VYSMEGACADIALYRLERSIQFSERVLPICLPDASHIILPPNTCHWISGMGSTQD 185
 Db 108 IVHQQFYITIQTG--ADIALEELPPVNISSRVHTVMLPASETFPPGMPCWTTGWDVDN 163
 Qy 186 GVPPLPHPTQLKLKVPIIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 241
 Db 166 DEPLPPPFPKVKVPMENHICDAKYHLGAYTGGDDYRIRDMCLAG--NSQRDSCKGD 223
 Qy 242 SGGLPLMCQVDGAWILLAGITSWGEBCAERNRPGYITISLAHSRWEKIV 289
 Db 224 SGGLPLVKYNTWLQAGVWSWDEGCAQPNRPGYTRVITYYLQDWHYY 269

RESULT 10 US-09-016-366A-19
 Sequence 19, Application US/09016366A
 Patent No. 5955431.

GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 ADDRESS: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 ZIP: 02210-2211
 COUNTRY: U.S.A.
 CITY: Boston
 STATE: MA
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELX:
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-016-366A-19

Query Match 30.8%; Score 529.5; DB 2; Length 273;
 Best Local Similarity 39.2%; Pred. No. 8.5e-45;
 Matches 113; Conservative 52; Mismatches 86; Indels 37; Gaps 9;

Query Match 30.8%; Score 529.5; DB 2; Length 273;
 Best Local Similarity 39.2%; Pred. No. 8.5e-45;
 Matches 113; Conservative 52; Mismatches 86; Indels 37; Gaps 9;

RESULTS 11
 US-08-978-404B-14
 Sequence 14, Application US/08978404B
 Patent No. 5968782

GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 NUMBER OF INVENTION: FIBRINOGEN
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,404B
 FILING DATE: 25-NOV-97
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,354
 FILING DATE: 04-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 5968782e
 US-08-978-404B-14

Qy 20 SLLLIASATLNAARIIPVPPACGPQLNRVYGGEDSTDSEWPNTSICKNG--THHCA 76
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 NLLLLALPVL-ASRAYAAAPGQALQRGVIGVQEAPPSKWPQVSLEVRHGPYMMHFCG 58
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 77 GSLIITSRWTAAHC---FKD-----NLUKPFLFSVLLGAQWLGNGPSSRSOKVGAWY 126
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 59 GSLIHPQWLTAAHVGPDKLAAVRQLEQRHAY-----YDQQLJPVSRI 105
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 127 EPHP-VYSMEKGACADIALYRLERSIQFSERVLPICLDPDASHLPPNTCHWISGWGSIQD 185
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 106 VHPHPEFTAGC-ADIALLEPEVNVSHVHTVTPPASETTPPGMCWVWTGWDVN 163
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 186 GPVLPHPQTOLKLKPVIDSEVCSHLYWRGAGQP---ITEDMLCAGYLEGERDACLGD 241
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 164 DERLPPPEPLKQVKVPMENHICDAKYHLGATYDDVRYDDMUCAG-NTRRDSCQGD 221
 :|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 242 SGPLMCMQDGAWLLAGITISWEGGAERNRPGVYISLSAHRSWKEIV 289
 :|||:|||:|||:|||:|||:|||:|||:|||:
 Db 222 SGGPLVKVNGTWLQAVVSNGECAQPNRPGIYTRVYTLWDWIHYV 266
 :|||:|||:|||:|||:|||:|||:|||:

RESULT 13
 US-08-978-404B-6
 ; Sequence 6, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978-404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 270;
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 5968782e
 ;
 US-08-978-404B-8

Qy 21 LLLIATATLNAARIIPVPPACGPQLNRVYGGEDSTDSEWPNTSICKNGT--HHCAG 77
 :|||:|||:|||:|||:|||:|||:|||:
 Qy 21 LLLIATATLNAARIIPVPPACGPQLNRVYGGEDSTDSEWPNTSICKNGT--HHCAG 77
 :|||:|||:|||:|||:|||:|||:

Db 4 LLILALPLFSLMHRSPLCQEWG----IVGGQEAPPNKWPQVSRLRANEYWRHFCCG 56
 ; SLIHPQWLTAAHC-----PKDNLNKPYLESVLGAQWLGNGPSSRSOKVGAWY 127
 ; Db 57 SLIHPQWLTAAHCVGPTIADPNKVRVQLRKQYL-----YDHLLAVRII 103
 ; Qy 128 PHPV-YSWKEGACADIALYRLERSIQFSERVLPICLDPDASHLPPNTCHWISGWGSIQD 186
 ; Db 104 THPTFYATQG--ADIALLELKKNPNNISSVHPVSLPASETFPSTGLCWVTTGMGNIDND 161
 ; Qy 187 VPLPHPQTOLKLKPVIDSEVCSHLYWRGAGQP---ITEDMLCAGYLEGERDACLGD 242
 ; Db 162 VSLPPPFPLREVQEVENQJCDKLYHKGYGTGDNLHIVRDDMLCAG-N8-HDSCQGDS 219
 ; Qy 243 GGPLMCMQDGAWLLAGITISWEGGAERNRPGVYISLSAHRSWKEIV 289
 ; Db 220 GGPLYCKVNCTWLQAVVSNGECAQPNRPGIYTRVYTLWDWIHYV 266
 ;
 RESULT 13
 US-08-978-404B-6
 ; Sequence 6, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978-404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273;
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 5968782e
 ;
 US-08-978-404B-6

Query Match 30.2%; Score 519.5; DB 2; Length 273;
 Best Local Similarity 37.3%; Pred. No. 8.4e-44;
 Matches 107; Conservative 57; Mismatches 86; Indels 37; Gaps 9;
 21 LLLIATATLNAARIIPVPPACGPQLNRVYGGEDSTDSEWPNTSICKNGT--HHCAG 77
 2 LKLILITPLLSSLVHAAPS LAMPRE-GIVGGQEASGNKPQVSRLRVNDTYWMHFCGG 59

Qy	78	SLLTRSWVITAACFKDN-----LNKPYLFSSVLGAWLQNGPGRSQRQKVYAWVE 1.27
Db	60	SLLHQLWLTAAHCYGPKNADPNKLRLQKLY-----YHDHLLTTSQII 106
Qy	128	PHP-VYSWKEGACADATLVRLESIQSERVYLPICLPDASTHLPPNTHCNISGWMSIQDG 1.86
Db	107	SHPDYIAQDG---ADIALLKLTNPNTNITSNVHTVSUPPASTFPSTGLCWTGWNINND 1.64
Qy	187	VPLPHPQTOLQKLKVPPLDSEVCSSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 2.42
Db	165	VSLPPPFPEBLBVQPVENRILCDLXHKGLNTGDNHVIRDDLMCAGN-EG-HDCQGDS 2.22
Qy	243	GGPLMCQVDGAWLIGLIISNGECCALRNRCGVYISLAHSRWSWEVKV 2.89
Db	223	GGPLVCKVEPTWLQGGSNGECCOPRNRCGVYISLAHSRWSWEVKV 2.69

Db	61	LJHPQWLTAACVGPVDADPNPKVRVOLRKVLY	-----	-YHDHLMTWSQSLIT	1.07
Qy	129	HP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDAISIHLPPNTICWISGMGSIQDG	187		
Db	108	HDPFYIVQDG - ADIALKLTKNPVNISDYYHVHPVLPASETTPSGTLCWVGTNGCNIDNGV	165		
Qy	188	PLPHPOTLQLKVPITDSEVCSSHLYWRGAGQGP - ITEDMLCAGYLEGERDACLGDSG	243		
Db	166	NBPPPFPLKEVQPTENHLCDLKYHKGLITGDNBVHTVRDDMLCAGN-EG-HDSCQGDSG	223		
Qy	244	GPLMCQVDGAWLLAGITSWGECAERNRPGVVTISLSAHRSWEVKIV	289		
Db	224	CPRVCKEKFDPDQGQGDNSSWCEGAGDQDCUTPMDPWTQDWHUWV	269		

RESULT 15
 US-09-016-366A-23
 Sequence 23, Application US/09016366A
 Patent No. 5955431
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 APPLICANT: Huang, Chifu
 TITLE OF INVENTION: MATRIX CELL PROTEASE PEPTIDE
 TITLE OF INVENTION: INHIBITORS
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-016-366A-23

	Query Match	Best Local Similarity	Score	DB 2;	Length 267;
Qy	32 AARIYPYPACGKPKQLNRRVYGGEDSDTSEPMVISIO---KNGTHICAGSLTSRNVITA 88	Matches 107;	Mismatches 51;	Pred. No. 2.5e-43;	Indels 35; Gaps
Db	5 ASRAYAAPGQALQRQGIVGGQEAPRSKWPQVSLRVRDRYWMHCGGSILTHPQWVLTA 64				
Qy	89 AHC----FKD-----NLNKPLPVFSVLLGANLGPNSRSRKGVAWEPIP-VVWKEG 137				
Db	65 AHCVGDPVKDLAALRVOLREOHL-----YQDQLPVSLIIVHQFTTAQIG 111				

Qy	138	ACADIALVRLETSQFESRVLPICLDPDASTHLLPPNTHCMWSGNGS1QDGYPLPHPTOLK	197
Db	112	-ADIALLEELPEPVKSSHVHTVLPASETFPQGMPCWNTGWDNDRLPFPFLRQ	169
Qy	198	LKVPIIDSEVCASHLYWRGAQGP -- ITEDMLCAGYLEGERDAQLGDSGGPLMQVDGA	253
Db	170	VKPKMENHICDAGHLGAYTGDDVIRDDMLCAG - NTRRDSQQGDSGGPLVQKVNGT	227
Qy	254	WILLAGLISWEGGCAERNRPGYIISLAHSRWEKIV	289
Db	228	WLQGVVSWEGGCAQPQNGRUYTTVYDWHIIHYV	263

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Job time: 722 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5	30	439.5	25.6	812	1	PLMS
OM protein - protein search, using sw model		31	437.5	25.4	367	2	JE0104
Run on:	August 29, 2002, 10:13:56 ; Search time 17.52 Seconds (without alignments)	32	437.5	25.4	437	2	S18407
Title:	US-09-903-925A-263	33	437.5	25.4	4548	1	S00657
Perfect score:	1720	34	437	25.4	263	1	KYRTB
Sequence:	MVSGAPPALGGGCLGFTS.....AQGGGALARPSQSSGAAARS 317	35	437	25.4	421	1	S11674
Scoring table:	BLOSUM62	36	434	25.2	265	2	T15451
	Gapop 10.0 , Gapext. 0.5	37	433.5	25.2	271	2	A25528
Searched:	283138 seqs, 96089334 residues	38	432.5	25.1	436	2	JX0172
Total number of hits satisfying chosen parameters:	283138	39	430.5	25.0	366	2	JE01058
Minimum DB seq length: 0		40	429.5	25.0	431	2	S47538
Maximum DB seq length: 2000000000		41	428	24.9	263	2	A21195
Post-processing: Minimum Match 0*	Maximum Match 100%	42	425	24.7	810	2	I46260
Database :	PIR_71;*	43	424.5	24.7	270	2	B29934
	2: Pir1;*	44	422	24.5	263	2	A31299
	3: Pir3;*	45	422	24.5	415	1	A34170
	4: Pir4;*						
ALIGNMENTS							
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A57014	prostasin (EC 3.4.21.-) precursor - human						
C;Species: Homo sapiens (man)							
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #Text_Change 18-Jun-1999							
C;Accession: A57014; A54866							
R;Yu, J.X.; Chao, L.; Chao, J.							
J. Biol. Chem. 270, 13483-13489, 1995							
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of prostasin							
A;Reference number: A57014; MUID:95286644							
A;Accession: A57014							
A;Status: translated from GB/EMBL/DDJB							
A;Molecule type: mRNA							
A;Residues: 1-343 <RES>							
A;Cross-references: GDB:676446; OMIM:600823							
A;Experimental source: prostate							
A;Note: Parts of this sequence were determined by protein sequencing							
R;Yu, J.X.; Chao, L.; Chao, J.							
J. Biol. Chem. 269, 18843-18848, 1994							
A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification							
A;Reference number: A54866; MUID:94308140							
A;Accession: A54866							
A;Molecule type: protein							
A;Residues: 45-64 <YUA>							
C;Genetics:							
C;Genes: GDB:PRSS8							
A;Cross-references: GDB:676446; OMIM:600823							
A;Map position: 16p11.2-16p11.2							
C;Superfamily: Prostasin; trypsin homology							
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein							
F;3-32/Domain: signal sequence #status predicted <SIG>							
F;33-44/45-343/Product: prostasin #status predicted <MAT>							
F;33-44/Domain: prostasin light chain #status predicted <CHL>							
F;45-54/3/Domain: prostasin heavy chain #status predicted <CHH>							
F;45-28/4/Domain: trypsin homology <TR>							
F;323-341/Domain: transmembrane #status predicted <TM11>							
F;37-154/70-86/168/244/201-223/234/262/disulfide bonds: #status predicted							
F;85-134/238/Active site: His, Asp, Ser #status predicted							
F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental							
Query Match Score 35.3%; Score 607.5; DB 1; Length 343;							
Best Local Similarity 44.28; Pred. No. 6.3e-44; Mismatches 108; Indels 13; Gaps 7;							
Matches 129; Conservative 42; Mismatches 108;							
QY 10 LGGGCLGTTSLL--LLASTAILNAAIRIPVPPACGKPOQLNRVYGGEDSTDSEWPWIVS 66							
Db 7 LGPQLQGAVAILLYGLRSGTGAEGARAP---CGVAFQA-RITGGSSAVAGWMPKQYS 61							
QY 67 IOKNGTHHAGSLLSLSRWVITAHHCFKDNLNKPFLSYLLGANOLGNPNSRSQKVGVAV 126							
Db 62 ITYEGVHWGGSLVSEQNVLSAAHCPESEHHKE-AYEVKLGAHQLDTSEDARYVSTLRDI 120							

Qy	1.27	EPPHYSWKEGACADIALVRERSIOPSERVAPICLLEDASIHLLPNTHCWIWGWSIDG	186
Db	1.21	IHPHSY-LQEGSQGDIAALLQSRPITSRYIRPICLDAANASPPNGJHCTVGWHAPS	179
Qy	1.87	VPLPHPQTQLKLKVPLIDSEVCSHLYWRGA-GQGP- ITEDMLCAGLEGERDACLGDSG	243
Db	1.80	VSLSPKPLQLEVPLISRETCNCLYNIDAKPPEPHVQEDMVCAGYVEGGKDACQGDSG	239
Qy	2.44	GPLMCOVDGAWLLAGTISWGEGCAERNRPGYYISLSAHRSSWEKIVGVQLR	295
Db	2.40	GPLSCPEGLMYLTGIVSWKGACGARNRPGYYTLASSAYSNOSKVNTEVOLP	291

PESULAT 2

Query Match	Score	DB 2;	Length	276;
Best Local Similarity	32.2%	Score 554;	DB 2;	Length 276;
Local Matches	41.6%	Pred. No.	1.7e-39	G
Matches	116;	Mismatches	93;	Indels 22;
Conservative	48;			

21	LLLIASTAILNARIAPIPVP - PACGKPQQLNRYGGEDSTDSENPWIVS1Q -- - KNGTHHCA	76
6	LLIWAWSLLASLIVYSAPRPA --- NORVIGVGHAESESKPWOISLRFKLNWIFFCG	61
77	GSLITSRWVITAACFKCDNLNKPLFYSVLLGAWQL - GNPGRSRSOKVGVANVEPHPVYSW	134
62	GSLIHPWNLTAACVGPBHKISQPLFRVOLREQQYLYGQD ----- QLJSLSNRITVPHPIXYT	116
Ddb	Ddb	Ddb

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RESULT 3
A32410 tryptase (EC 3.4.21.59) precursor - dog
Species: Canis lupus familiaris (dog)
Date: 12-Oct-1989 #sequence_revision 12-Oct-1989
C: Accession #: A32410
C: Venderstiel, P.; Craik, C.S.; Nidel, J.A.; Caughey, G.H.
C: Biochemistry 28: 4148-4155, 1989
A: Molecular cloning of dog mast cell trypsin and a related protease
A: Reference number: A32410; MUID: 83152460

A molecule type: unknown
 A; Residues: I1275<VAN>
 A; Cross-references: GB:M24664; NID:9163982; PIDN:AAA30854.1; PID:9163983; G
 C; Superfamily: trypsin homology
 C; Keywords: hydrolase; serine proteinase; zymogen
 E; 1-21/Domain: signal sequence #status predicted <SIG>
 E; 22-30/Domain: activation peptide #status predicted <ACT>
 E; 31-275/Product: trypsin #status predicted <MAT>
 F; 31-26/Domain: trypsin homology <TRY>
 F; 74-121/224/Active Site: His, Asp, Ser #status predicted

Query Match	Score	DB 2;	Length
Best Local Similarity	31.7%	546;	275;
	40.9%	Pred. No.	Be-39;

23	QY	LLASTAILNAAARTFPPVPPACGGKPQOLNRRVGGEDSTDSEPVIVTSTOKNG--THHAGSL	79	
	Dbb	1 : : : : : : : : : : : : : : : : : :	5 LVALALLGSL-VPSPAPGQALQRGVITGGREAPGSKWPQSVLRLKQYWRHICGGSL	63
80	QY	LTSRWRVITAACFKDNKPLFSLVLLGAWOLGNPNSRSQKVGYAWVEPHVYWSKEGAC	139	
	Dbb	1 : : : : : : : : : : : : : : : : : :	64 IHPQWVLIAAHCYGPNVCPCEIRVQLRQEHL--YYQDHLLPWNRYHMPNTYPENG-	119
140	QY	ADIALVRLERSTQSERYLPICLDASIHLPNTHCWISGWGSLSQDGVLPLPHPTQLKL	199	
	Dbb	1 : : : : : : : : : : : : : : : : :	120 ADFALELEDPVNVAHVQPVTLPPALQTFTPTGPMCPWYTGWGDYHSCTPLPPPFPLQVK	179
200	QY	VPIIDSEYCSHLYWRAGQGP--ITEDMLCACYLEGERDACLGDGSQGPLMCQYDGAML	255	
	Dbb	1 : : : : : : : : : : : : : : : : :	180 VPIVENSMCDVQYFHGLSTGDGVIRVEDMLCAG--NSKSDSCQDSGSPPLCYRCRYRGVWL	237
256	QY	LAGISWEGGCAERNRPGYIISLSAHRSHKEIV	289	
	Dbb	1 : : : : : : : : : : : : : : : : :	238 QASVQSWGFGC&DPNPDGIVYTMVAVVIVDMTHQVW	271

RESULT 4
JJC4171
tryptase (N)
Alternat-
ive C; Species:
C; Date: 27
Accession
Number: RIDEH;
Title: Biochem
Reference:

A;Accession: JC4171 A;Molecule type: mRNA A;Residues: 1-274 <IDE> C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is up elease inhibitors. C;Superfamily: trypsin; trypsin homology C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen F;1-19/Domain: signal sequence #status predicted <SIG> F;20-24/Domain: activation peptide #status predicted <ACT> F;25-29/Domain: product; mast cell tryptase #status predicted <PROD> F;30-266/Domain: trypsin homology <TRY> F;73,120,223/Active site: His, Asp, Ser #status predicted F;131/Binding site: carbohydrate (Asn) (covalent) #status predicted	Query Match 31.3%; Score 538.5; DB 2; Length 274; Best Local Similarity 40.6%; Pred. No. 3.4e-38; Gaps 10; Matches 117; Conservative 46; Mismatches 84; Indels 41; Gaps 10;	QY 116 SRSQKVGVAWEPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLDPASITHLPPNTH 174 Db 59 YQDQLLPSPRIIPHNCVSVKNG-ADIALEDDKLKVNTSWHYPQPVTEPESETFPPTQ 116
		QY 175 CWISWGGSSTODGVYPLPHQTLQKVKPILSEVCSHLWKGAGQGP---ITEDMLCAGY 230 Db 117 CWTGWMGNDNGRLLPFPKVKPVTVNSYCDRKTHSGLSTGDNVPIVREDMLCAG- 175
		QY 231 LEGERDACLGDSGQPLMQLQVDGAMLLAGLISWEGCAERNRPGWY ISVSAHRSWVEKIV- 289 Db 176 -DSGRNFEQGDSGQPLVCKVNGTFLQasvSNEDGCAKPNRPGTYTRVTSYLDWIHQVYP 234
		QY 290 QG 291 Db 235 QG 236
	RESULT 6 A45754	QY 21 LLLIATST---A1LNAAARIPIPAPAGKPKQQLNRYVGGEDSTDSEWPWYISQKNGT--HH 74 Db 5 LLLIALLSPASLYHAAPCPVKQRYG-----IVGGRASESKWPMQYSLRFKFSEFWMF 57
		QY 75 CAGSLLTSEWVTAAHCFKDNLNKPYLPSVLLSAWQLNPGSSQ-----KVEVAV 125 Db 58 CGGSUHSPQWVLTAAHCVGVLHKSPELFRVQI-----REQLYYADQLLTVNARTV 107
		QY 126 VEPHPVSYWKEGACADIALVRLERSIQFSERVLPICLDPASITHLPPNTHCWISWGGSSTQD 185 Db 108 VHPH-YTTEVEDG--ADIALELETPVNVSTHIPSLEPASETEPSGTSCTSWVIGWDIDS 164
		QY 186 GVPLPHQTLQKVKPILSEVCSHLWKGAGQGP---PITED-MICAGYLEGERDACLGD 241 Db 165 DEPLLPPLPKQVKPVTNSCDRKYHTGLTDYDPIVQDGMLCAG--NTRSDSCQGD 222
		QY 242 SGGLPLMCQVDGAWLLAGLISWEGCAERNRPGWY ISVSAHRSWVEKIV 289 Db 223 SGGLPLVKYKGTWQAGVWSGGCAEANRPGTYTRVYLLDWHRYV 270
	RESULT 5 S68702	QY 200 SLLLASTAILNARIPVPPACGKPKQQLNRYVGGEDSTDSEWPWIVSTQ---KNGTHHCA 76 Db 3 SLLILALPLV---ASRAYPAVQYQALQAGIVGQEARSRSKWNQVSRVDRYWWHRCG 60
		QY 200 SLLLASTAILNARIPVPPACGKPKQQLNRYVGGEDSTDSEWPWIVSTQ---KNGTHHCA 76 Db 3 SLLILALPLV---ASRAYPAVQYQALQAGIVGQEARSRSKWNQVSRVDRYWWHRCG 60
		QY 277 GSLLITSPWVITAAHCFCNKNPKPLFSLVLLGQNLGNPG---RSQKVGVAWEPHP-V 131 Db 61 GSLLIHPQWVLTAAHCGLGDKVLDLATLRV-----NSGTHLXYQDQQLPVSVIMVHFQ 112
		QY 132 YSWKEGACADIALVRLERSIQFSERVLPICLDPASITHLPPNTHCWISWGMSIDQGVPLPH 191 Db 113 YIQTG-ADIALELETPVNTSRVHVMPLPASETPPPGMICWVTPGVDVNDDEPP 170
		QY 192 PQLQKVKPILSEVCSHLWKGAGQGP---ITEDMLCAGYLEGEDACLGDSGGPLM 247 Db 171 PFPBKQVKPIMENHICAKYHLGAYTSDDVRLTRDDMLCAG--NSORDSCKGDSGGPLV 228
		QY 248 CGDGLVWQVLSWEGGAERNRPGWY ISVSAHRSWVEKIV 289 Db 229 CKVNGTFLWQGVVSWEDECAQPNRPGTYTRVYLLDWHYHV 270

Query Match 31.2%; Score 536; DB 2; Length 237;
Best Local Similarity 42.6%; Pred. No. 4.7e-38;
Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;
A;Accession: S68702
A;Molecule type: protein
A;Residues: 1-237 <PAL>
A;Cross-references: EMBL:X94982; NID:91332446; PIDN:CAA64438.1; PID:g1332447
A;Accession: S6876
A;Molecule type: protease
A;Residues: 1VGGQPA/1-8,61-74,90-97,126-148;162-190;208-222;227-235 <PAW>
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
F;1-229/Domain: trypsin homology (fragment) <TR1>
F;36-83,177/Active site: His, Asp, Ser #status predicted
F;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.2%; Score 536; DB 2; Length 237;
Best Local Similarity 42.6%; Pred. No. 4.7e-38;
Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;
A;Accession: S68702
A;Molecule type: protein
A;Residues: 1VGGQPA/1-8,61-74,90-97,126-148;162-190;208-222;227-235 <PAW>
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
F;1-229/Domain: trypsin homology (fragment) <TR1>
F;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.2%; Score 536; DB 2; Length 237;
Best Local Similarity 42.6%; Pred. No. 4.7e-38;
Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;
A;Accession: S68702
A;Molecule type: protein
A;Residues: 1VGGQPA/1-8,61-74,90-97,126-148;162-190;208-222;227-235 <PAW>
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
F;1-229/Domain: trypsin homology (fragment) <TR1>
F;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.3%; Score 538.5; DB 2; Length 274;
Best Local Similarity 40.1%; Pred. No. 1.2e-37;
Matches 113; Conservative 50; Mismatches 93; Indels 26; Gaps 8;
A;Accession: S68702
A;Molecule type: protein
A;Residues: 1-237 <PAL>
A;Cross-references: EMBL:X94982; NID:91332446; PIDN:CAA64438.1; PID:g1332447
A;Accession: S6876
A;Molecule type: protease
A;Residues: 1VGGQPA/1-8,61-74,90-97,126-148;162-190;208-222;227-235 <PAW>
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
F;1-229/Domain: trypsin homology (fragment) <TR1>
F;36-83,177/Active site: His, Asp, Ser #status predicted
F;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.3%; Score 538.5; DB 2; Length 274;
Best Local Similarity 40.6%; Pred. No. 3.4e-38; Gaps 10;
Matches 117; Conservative 46; Mismatches 84; Indels 41; Gaps 10;
A;Accession: JC4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is up elease inhibitors.
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-24/Domain: activation peptide #status predicted <ACT>
F;25-29/Domain: product; mast cell tryptase #status predicted <PROD>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.3%; Score 538.5; DB 2; Length 274;
Best Local Similarity 40.6%; Pred. No. 3.4e-38; Gaps 10;
Matches 117; Conservative 46; Mismatches 84; Indels 41; Gaps 10;
A;Accession: JC4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is up elease inhibitors.
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-24/Domain: activation peptide #status predicted <ACT>
F;25-29/Domain: product; mast cell tryptase #status predicted <PROD>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;131/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT	7	8
B35863	A35863	A35863
trypsinase (EC 3.4.21.59) II precursor - human	trypsinase (EC 3.4.21.59) I precursor - human	trypsinase (EC 3.4.21.59) I precursor - human
N; Alternative names: trypsin; trypsin beta	C; Species: Homo sapiens (man)	C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)	C; Date: 12-Oct-1990 #sequence-revision 12-Oct-1990 #text_change 21-Jul-2000	C; Date: 12-Oct-1990 #sequence-revision 12-Oct-1990 #text_change 21-Jul-2000
C; Date: 03-Feb-1994 #sequence-revision 03-Feb-1994 #text_change 21-Jul-2000	C; Accession: B35863; A37193; 159473	C; Accession: B35863; A37193; 159473
R; Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990	A; Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A; Reference number: A35863; MUID:90251647	A; Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A; Reference number: A35863; MUID:90251647
A; Accession: B35863	A; Accession: B35863	A; Accession: B35863
A; Molecule type: mRNA; DNA Residues: 1-275 <VAN>	A; Molecule type: mRNA Residues: 1-275 <VAN>	A; Molecule type: mRNA Residues: 1-275 <VAN>
A; Cross-references: GB:M33492; NID:q339982; PIDN:AAA36779.1; PID:q339983	A; Cross-references: GB:M33492; NID:q339982; PIDN:AAA36779.1; PID:q339983	A; Cross-references: GB:M33491
A; Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic R; Miller, J.S.; Moxley, G.; Schwartz, L.B.	A; Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic R; Miller, J.S.; Moxley, G.; Schwartz, L.B.	R; Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Clin. Invest. 86: 864-870, 1990	A; Title: Cloning and characterization of a second complementary DNA for human trypsinase.	J. Leukoc. Biol. 47: 409-419, 1990
A; Reference number: A37193; MUID:90369005	A; Accession: A37193	A; Title: Purification of trypsinase from a human mast cell line.
A; Accession: A37193	A; Accession: A37193	A; Reference number: A60939; MUID:90244210
A; Molecule type: mRNA Residues: 1-275 <HIL>	A; Molecule type: protein Accession: A60939	A; Molecule type: protein Residues: 31-38, 'P', '40-41, 'X', '43, 'T', '45-48, 'X', '50 <BUT>
A; Cross-references: GB:M37488; NID:9179583; PIDN:AAA51843.1; PID:q179584	A; Cross-references: GB:M37488; NID:9179583; PIDN:AAA51843.1; PID:q179584	A; Residues: 31-38, 'P', '40-41, 'X', '43, 'T', '45-48, 'X', '50 <BUT>
Scand. J. Immunol. 37: 203-208, 1993	A; Title: Characterization of a trypsinase mRNA expressed in the human basophil cell line K	A; Note: 44-Gly was also found R; Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien J. Biol. Chem. 262: 1363-1373, 1987
A; Reference number: 159473; MUID:93166209	A; Status: preliminary; translated from GB/EMBL/DBJ	A; Title: Human pituitary trypsinase: molecular forms, NH-2-terminal sequence, immunocyt A; Reference number: A39326; MUID:87109258
A; Accession: A39326	A; Accession: A39326	A; Reference number: A39326; MUID:87109258
A; Molecule type: protein Residues: 1-275 <RES>	A; Molecule type: protein Residues: 31-38 <CRO>	A; Molecule type: protein Residues: 31-38 <CRO>
A; Experimental source: basophil cell line KU812 Genetics:	A; Experimental source: pituitary Genetics:	A; Experimental source: pituitary Genetics:
A; Gene: GPS1	A; Introns: 21/1: 78/2; 177/1; 221/3	A; Introns: 21/1: 78/2; 177/1; 221/3
A; Cross-references: GDB:125890; OMIM:191080	C; Superfamily: trypsin; trypsin homology	C; Superfamily: trypsin; trypsin homology
A; Map Position: 16pter-16pter	C; Keywords: hydrolase; serine protease; zymogen	C; Keywords: hydrolase; serine protease; zymogen
C; Key words: trypsin; trypsin homology; zymogen	F; 1-21/Domain: signal sequence #status predicted <SIG>	F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 1-21/Domain: signal sequence #status predicted <ACT>	F; 22-30/Domain: activation peptide #status predicted <ACT>	F; 22-30/Domain: activation peptide #status predicted <ACT>
F; 31-275/Product: trypsinase I #status experimental <MAT>	F; 31-275/Product: trypsinase I #status experimental <MAT>	F; 31-275/Domain: trypsin homology <TRY>
F; 31-275/Domain: trypsinase II #status predicted <ACT>	F; 74,121/224/Active site: His, Asp, Ser #status predicted	F; 74,121/224/Active site: His, Asp, Ser #status predicted
F; 74,121/224/Active site: His, Asp, Ser #status predicted	Query Match Score 30.8%; Best Local Similarity 39.2%; Matches 113; Conservative 53; Mismatches 53; Indels 37; Gaps 9;	Query Match Score 30.8%; Best Local Similarity 39.2%; Pred. No. 2e-37; Mismatches 52; Indels 37; Gaps 9;
Db 20 SLLILASTAILNAARIARIPVPPACGKPKQOLNVRVGGEDSTDSEWPWIVSTOKNG --THHCA 76	Db 20 SLLILASTAILNAARIARIPVPPACGKPKQOLNVRVGGEDSTDSEWPWIVSTOKNG --THHCA 76	Db 20 SLLILASTAILNAARIARIPVPPACGKPKQOLNVRVGGEDSTDSEWPWIVSTOKNG --THHCA 76
Db 3 NLLIALPVL--ASRAYAAPGAPGALQRVGVQQEAPRSKWQVSLSRVRHGTWMMHFCG 60	Db 3 NLLIALPVL--ASRAYAAPGAPGALQRVGVQQEAPRSKWQVSLSRVRHGTWMMHFCG 60	Db 3 NLLIALPVL--ASRAYAAPGAPGALQRVGVQQEAPRSKWQVSLSRVRHGTWMMHFCG 60
Qy 77 GSLLTSRWVYTAAHC---FKD----NLUKPYLFSVLLGAQLGNPGSRSOKVGYAWV 126	Qy 77 GSLLTSRWVYTAAHC---FKD----NLUKPYLFSVLLGAQLGNPGSRSOKVGYAWV 126	Qy 77 GSLLTSRWVYTAAHC---FKD----NLUKPYLFSVLLGAQLGNPGSRSOKVGYAWV 126
Db 61 GSLIHPQWVLTAAHCVGPDVKDLAALRYQLREQLY-----YQDQILPISRI 107	Db 61 GSLIHPQWVLTAAHCVGPDVKDLAALRYQLREQLY-----YQDQILPISRI 107	Db 61 GSLIHPQWVLTAAHCVGPDVKDLAALRYQLREQLY-----YQDQILPISRI 107
Qy 127 EPHP-VYSWEKGACADIALYLERSIQPSERVLICLPPDAISIHLPPNTHCWLSGWGSTQD 185	Qy 127 EPHP-VYSWEKGACADIALYLERSIQPSERVLICLPPDAISIHLPPNTHCWLSGWGSTQD 185	Qy 127 EPHP-VYSWEKGACADIALYLERSIQPSERVLICLPPDAISIHLPPNTHCWLSGWGSTQD 185
Db 108 IVHPQFYTQIG--ADIALLEELPEPVKVSSHVHTVLPASERFPFGMPCWNTGWGDVDN 165	Db 108 IVHPQFYTQIG--ADIALLEELPEPVKVSSHVHTVLPASERFPFGMPCWNTGWGDVDN 165	Db 108 IVHPQFYTQIG--ADIALLEELPEPVKVSSHVHTVLPASERFPFGMPCWNTGWGDVDN 165
Qy 186 GPVLPHPQTQLKVPIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 241	Qy 186 GPVLPHPQTQLKVPIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 241	Qy 186 GPVLPHPQTQLKVPIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 241
Db 166 DERLPPPFPIQKVSPIMENHICAKYHILGAYGDDVRDMLCAG--NTRRDSCQGD 223	Db 166 DERLPPPFPIQKVSPIMENHICAKYHILGAYGDDVRDMLCAG--NTRRDSCQGD 223	Db 166 DERLPPPFPIQKVSPIMENHICAKYHILGAYGDDVRDMLCAG--NTRRDSCQGD 223
Qy 242 SGGLPMCOVQDGWMLLAGISWGEGCCAERNPGYIISLSAHSRSHVEKIV 289	Qy 242 SGGLPMCOVQDGWMLLAGISWGEGCCAERNPGYIISLSAHSRSHVEKIV 289	Qy 242 SGGLPMCOVQDGWMLLAGISWGEGCCAERNPGYIISLSAHSRSHVEKIV 289
Db 224 SGGLPLVCKVNGTWLQAGVYSWGECCAQPNRPGTYTRVYYLDWTTHHYV 271	Db 224 SGGLPLVCKVNGTWLQAGVYSWGECCAQPNRPGTYTRVYYLDWTTHHYV 271	Db 224 SGGLPLVCKVNGTWLQAGVYSWGECCAQPNRPGTYTRVYYLDWTTHHYV 271
RESULT	9	C35863

	F;26-262/Domain: trypsin homology <TRY>
C;Species: Homo sapiens (man)	
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Jun-2001	
C;Accession: C35863; A35863; A35863; A35863	Query Match 30.3%; Score 522; DB 2; Length 270; Best Local Similarity 38.0%; Pred. No. 8 5e-37; Mismatches 109; Conservative 52; Indels 42; Gaps 9;
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.	QY 21 LLLIASTAILNAARIPVPPACGKPKQLNRRVGGEDSTDSEMPWIVSICKNGT---HHCAG 77
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990	A;Accession: C35863; MUID:30251647
A;Title: Human mast cell trypsin: multiple cDNAs and genes reveal a multigene serine proteinase family	A;Accession: C35863
A;Molecule type: mRNA	A;Molecule type: mRNA
A;Residues: 9-275 <VAN>	A;Residues: 9-131, K, 132-275 <VA2>
A;Accession: A35863	A;Cross-references: GB:M33493; NID:9339984; PIDN:AA36780_1; PID:9339985
A;Molecule type: DNA	C;Superfamily: trypsin; trypsin homology
A;Residues: 1-9 <VA2>	C;Keywords: hydrolase; serine protease; zymogen
A;Cross-references: GB:M33494; NID:93927804; PIDN:AC83172_1; PID:9339977	F;1-21/Domain: signal sequence #status predicted <SIG>
A;Note: the first nine residues of this sequence are inferred from genomic DNA of trypsin submitted to GenBank, April 1990	F;22-30/Domain: activation peptide #status predicted <ACT>
A;Reference number: A38893	F;31-275/Domain: trypsin I #status predicted <MAT>
A;Accession: A38893	F;31-267/Domain: trypsin homology <TRY>
A;Molecule type: mRNA	F;74-121,224/Active site: His, Asp, Ser #status predicted
A;Residues: 9-131, K, 132-275 <VA2>	
A;Accession: A35863	
A;Molecule type: DNA	
A;Residues: 1-9 <VA2>	
A;Cross-references: GB:M33494; NID:9339984; PIDN:AA36780_1; PID:9339985	
A;Superfamily: trypsin; trypsin homology	
C;Keywords: hydrolase; serine protease; zymogen	
F;1-21/Domain: signal sequence #status predicted <SIG>	
F;22-30/Domain: activation peptide #status predicted <ACT>	
F;31-275/Domain: trypsin homology <TRY>	
F;74-121,224/Active site: His, Asp, Ser #status predicted	
RESULT 11	
A47246	tryptase (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)	C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000	C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
R;McNeil, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.	R;McNeil, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992	Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast cell tryptase	A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast cell tryptase
A;Reference number: A47246; MUID:93087489	A;Reference number: A47246; MUID:93087489
A;Accession: A47246	A;Accession: A47246
A;Molecule type: nucleic acid	A;Molecule type: nucleic acid
A;Residues: 1-273 [MCN]>	A;Residues: 1-273 [MCN]>
A;Cross references: GB:LO0653; NID:g200518; PIDN:AAA39992_1; PID:g200519	A;Cross references: GB:LO0653; NID:g200518; PIDN:AAA39992_1; PID:g200519
A;Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBIPI:119746)	A;Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBIPI:119746)
C;Superfamily: trypsin; trypsin homology	C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine protease	C;Keywords: hydrolase; serine protease
F;29-265/Domain: trypsin homology <TRY>	F;29-265/Domain: trypsin homology <TRY>
Query Match 30.4%; Score 522.5; DB 2; Length 275; Best Local Similarity 38.9%; Pred. No. 7.8e-37; Mismatches 87; Indels 37; Gaps 9;	Query Match 30.1%; Score 518; DB 2; Length 273; Best Local Similarity 38.5%; Pred. No. 1.9e-36; Mismatches 110; Conservative 53; Indels 38; Gaps 9;
QY 20 SLLIASTAILNAARIPVPPACGKPKQLNRRVGGEDSTDSEMPWIVSICKNGT---KNGTHHCA 76	QY 22 LLLIASTAILNAARIPVPPACGKPKQLNRRVGGEDSTDSEMPWIVSICKNGT---HHCAGS 78
Db 3 NLLILALPVL-ASRAYAAPGQALQRGVTVGGQEAAPSKWVQSLRVRDRYWMHFCG 60	Db 4 LLILITLPLSSL--VHAAPGAPMTREGVGGQEAHGRKWPWQSLRNDTYMHFCGCS 60
QY 77 GSLITSRWVITAAC---FKD----NLNKPVLFSVLLGAWQLGNPGSRQKVGA 126	QY 79 LLITRWVITAAC---FKDNLNKPVLFSVLLGAWQLGNPGSRQKVGA 128
Db 61 GSLIHPQWVLTAAHCVGDPVKDLAALRVOLREQLY-----YQDQQLPVSR 107	Db 61 LIHQWVLTAAHCVGDPVKDLAALRVOLREQLY-----YHDHLMVTSQIT 107
QY 127 EPHP-VYSNKEGACADIALYRLERSIQSERVLPICLPDASHLPPNTHCWISGWGSTQD 185	QY 129 HP-VYSNKEGACADIALYRLERSIQSERVLPICLPDASHLPPNTHCWISGWGSTQD 187
Db 108 IVHPFQYTAQG-ADIALELERPVNVSHTVTLPASETEPPGMPCWTVGWGDVDN 165	Db 108 HPDYTVQD-ADIALELERPVNVSHTVTLPASETEPPGMPCWTVGWGDVDN 165
QY 186 GPVLPHPOTLQKLKVPIIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDAUCJGD 241	QY 188 PLPHPOTLQKLKVPIIDSEVCSHLYWRGAGQGP---ITEDMLCAGYLEGERDAUCJGD 243
Db 166 DERLPPPFPLKQKVPMENHICDAKYHUGAYTSDDVRYRVDMLCAG - NTRRDSQGD 223	Db 166 NLPPPFPLKQKVPMENHICDAKYHUGAYTSDDVRYRVDMLCAG - NTRRDSQGD 223
QY 242 SGPILMCQVGDGAWLLAGIISWSEGCAERNRPGYYISLSAHRSSWEKIV 289	QY 244 GPLMCQVGDGAWLLAGIISWSEGCAERNRPGYYISLSAHRSSWEKIV 289
Db 224 SGGPLVCKVNTWLQAVVSWGECAQPNRGIYTRVITYLDWIHHYV 271	Db 224 GPLVCKVNTWLQAVVSWGECAQPNRGIYTRVITYLDWIHHYV 269
RESULT 10	
S56160	mast cell trypsin precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)	C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 21-Nov-1995 #sequence_revision 03-Nov-1995	C;Date: 21-Nov-1995 #sequence_revision 03-Nov-1995
C;Accession: S56160	C;Accession: S56160
R;Marakumi, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N	R;Marakumi, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N
Biochem. J. 309, 921-926, 1995	Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell trypsinase of Mongolian gerbil, Meriones u	A;Title: Cloning of the cDNA encoding mast cell trypsinase of Mongolian gerbil, Meriones u
A;Accession: S56160	A;Accession: S56160
A;Status: preliminary	A;Status: preliminary
A;Molecule type: mRNA	A;Molecule type: mRNA
A;Residues: 1-270 <MR>	A;Residues: 1-270 <MR>
C;Superfamily: trypsin; trypsin homology	C;Superfamily: trypsin; trypsin homology

Qy	49	RVVGGEDSTDSEWPWIVSIQ -- KNGTHHAGSLLTSRWWVITAHHCFKDNLNKPVLFSVL	105
Db	390	RIVGGINSSLGEWPWIVSIQYKLVSONHMCGGSIIGRNWLTAHCF - DGIPYPDVRIY	448
Qy	106	LGAWQLGNPGSRQSKYGVAVVWEPHPVYSKEGACADIALYRLERSIQFSSERVLPICLPDA	165
Db	449	GGILNLSSETNKTTPFSSIKELLIHQKYKMSSEGSD-YDIALKLQTPLNTEFQKPICLPSK	507
Qy	166	SIHLPPNTHCMWSGNSIQDGVPLPHPTOLQKLPITDSEVCSHLYWRGAGQGPITEM	225
Db	508	ADNTTYYTNWVNTGNOYTKERGETON - IIQKATIPLVPEECORKY --- RDYVITKQM	561
Qy	226	LCAGYLEGERDACLGSGGPLMCQVDGAWILLAGITISWGECACERNRPGYIISLAHRSNW	285
Db	562	ICAGIKEGGIDACKGDSGGBLVCKHSGRWQLVGTISWGECACRQECPGVYTAKVEYIDW	621
Qy	286	EKIVQEVQLR	295
Db	622	LEKIQSSKER	631

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1720	100.0	317	1	BSS4_HUMAN	Q9zrn4	homo sapien
2	1270	73.9	306	1	BSS4_MOUSE	Q9ar10	mus musculu
3	739	43.0	290	1	MNP_HUMAN	Q9gr3	homo sapien
4	607.5	35.3	343	1	PSSB_HUMAN	Q16651	homo sapien
5	578.5	34.0	342	1	PSSB RAT	Q9gs87	rattus norvegicus
6	578.5	33.6	273	1	TRYT_SHEEP	Q9sdi2	ovis aries
7	574.5	33.4	342	1	PSSB MOUSE	Q9rsd1	mus musculu
8	559	33.1	321	1	TRYG_HUMAN	Q9rr2	homo sapien
9	554	32.2	276	1	MCT6_MOUSE	P21845	mus musculu
10	546	31.7	275	1	TRYT_CANFIA	P15444	canis familiaris
11	538.5	31.3	274	1	MCT6 RAT	P50343	rattus norvegicus
12	532.5	31.0	275	1	TRYT_PIG	Q912d1	sus scrofa
13	531.5	30.9	314	1	TEST_HUMAN	Q96m0	homo sapien
14	530.5	30.8	275	1	TRB2_HUMAN	P20231	homo sapien
15	530	30.8	324	1	TEST_MOUSE	Q91hj7	mus musculu
16	529.5	30.8	275	1	TRYA_HUMAN	Q15661	homo sapien
17	526.5	30.6	275	1	TRYT_RAT	P15157	homo sapien
18	522	30.3	270	1	TRYT_MERLIN	P50342	meriones unicolor
19	519.5	30.2	273	1	MCT7_RAT	P21435	rattus norvegicus
20	519	30.2	311	1	TRYG MOUSE	Q9qul7	mus musculu
21	518	30.1	273	1	MCT7_MOUSE	Q08844	mus musculu
22	490.5	28.5	455	1	TMS5_MOUSE	Q9r04	mus musculu
23	482.5	28.1	457	1	TMS5_HUMAN	Q913s3	homo sapien
24	481	28.0	638	1	KAL_HUMAN	P03951	homo sapien
25	475.5	27.6	625	1	FA11_HUMAN	P03951	homo sapien
26	472	27.5	638	1	KAL_MOUSE	P22622	mus musculu
27	472.5	27.5	437	1	TMS4_HUMAN	Q9ar34	homo sapien
28	472.5	27.5	454	1	TMS3_HUMAN	P57127	homo sapien
29	469.5	27.3	638	1	KAL RAT	P14272	rattus norvegicus
30	463	26.9	416	1	HEPS_MOUSE	Q3453	mus musculu
31	462	26.9	492	1	TMS2_HUMAN	Q11393	homo sapien
32	460.5	26.8	812	1	PLMN_BOVIN	P08668	bos taurus
33	457.5	26.6	1034	1	ENTK_PIG	P98074	sus scrofa

ALIGNMENTS

RESULT	1						
ID	BSS4_HUMAN	STANDARD;	PRP;	317 AA.			
AC	Q9zrn4; Q43342;						
DT	16-OCT-2001 (Rel. 4.0, Created)						
DT	16-OCT-2001 (Rel. 4.0, Last sequence update)						
DT	16-OCT-2001 (Rel. 4.0, Last annotation update)						
DE	Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)						
DE	(SP001LA).						
GN	PRSS22 OR PRSS22 OR BSSP4.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
NCBI_TaxID	9006;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Brain.						
RA	Mitsui S., Okui A., Koninami K., Yamaguchi N.;						
RT	"Cloning and characterization of a human brain-specific serine protease, hBSP-4";						
RT	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.						
RL	[2]						
RN							
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Pancreas;						
RA	Wong G.W., Stevens R.L.;						
RA	"Identification of a new member of the chromosome 16 family of serine proteases.";						
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.						
RL	[3]						
RN							
RP	SEQUENCE OF 47-317 FROM N.A.						
RC	"Cloning and characterization of a new member of the chromosome 16 family of serine proteases.";						
RA	Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E., Robinson D.O., Jones M., Buckingham J., Chatstee L., Thompson S., Meinicke L., Longmire J., White S., Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S., Ueng S., Tatum O., Campbell C., Fawcett J., Deaven L.;						
RA	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.						
RL	-!- SIMILARITY: BELONGS TO THE PEPTIDEASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.						
CC							
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CC							
CC							
CC							
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CC							
CC							
CC							
DR	EMBL; AR01079; BAB2033.1; -;						
DR	EMBL; AF321152; AAG35070.1; -;						
DR	EMBL; AC003955; AAB93671.1; -;						
DR	MEROPS; S01_552; -;						
DR	InterPro; IPR001314; Chymotrypsin.						
DR	InterPro; IPR001254; Trypsin.						
DR	Pfam; PF00089; Trypsin_1.						
DR	PRINTS; PRO0722; CHYMOTRYPSIN.						
DR	SMART; SM00020; Tryp_Spo; 1.						
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.						

RL	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC	-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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CC	EMBL: At30653; CAC35467.1; -.
DR	MEROPS; S01_074; -.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR001254; Trypsin.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; TRYPT_SP; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
DR	KW Hydrolyase; Serine protease; zymogen; Signal; Glycoprotein.
FT	SIGNAL 1 22
FT	PROPEP 23 34
FT	CHAIN 35 290
FT	DOMAIN 35 277
FT	ACT_SITE 75 75
FT	ACT_SITE 124 124
FT	ACT_SITE 229 229
FT	DISULFID 60 76
FT	DISULFID 158 235
FT	DISULFID 191 214
FT	DISULFID 225 253
FT	CARBOHYD 55 55
FT	CARBOHYD 79 79
SQ	SEQUENCE 290 AA; 31940 MW; 67BDC93EC70BFF7 CRC64;
Query Match	43.0%; Score 739; DB 1; Length 290;
Best Local Similarity	48.8%; Pred. No. 1..le-56;
Matches	139; Conservative 49; Mismatches 87; Indels 10; Gaps 4;
QY	21 LILLIASTATIINAAARIIPVPPAACGEGQQLNRRVGGEDSDTSEWPWIVTISKNGTHCAGSLI 80
Db	10 LILLIC---FGSOPAKATAAGPRPRMNVGQDQTSPQRNGSHFCGCSLI 65
QY	81 TSMWVITAAHCFDNLKPKYLPSVYLLGAWLGNPGRSQRSVWKGACAA 140
Db	66 AEQWLVTAACFR NTSETSLXQVLLGARQWQGPHAMYARQVOVESNPLQ-GTASSA 123
QY	141 DIALYRLEFSQSERVLICLDASILHPLPHDTQLKLV 200
Db	124 DVALVEELAPVPPFTNYILPVCLDPSPVTFETGNWCWGTGWSPEEDLLEPRILQKLAV 183
QY	201 PTDSEVCSSHLYWRGAGQ---PITEDMLCAGYLEGERDACLGDGSGLPMLCCYDGAWLL 256
Db	184 PTDTPKCNLIXYSKDTEGYQPKTKNDMCACFEGRKDACKGDSGCCPLVLGQSMLQ 243
QY	257 AGISWGECCAEERNRPGVYIISLSAHRSMYEKTYOGYOLRGRAGGG 301
Db	244 AGVISWGECCARQNRPGVYIRVTAAHHNWLRPLKQFQPARIQGG 288
RESULT	4
ID	PSS8_HUMAN
AC	Q16651; Q9UCA3;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Prostasin precursor (EC 3.4.21.-).
GN	PRSS8.
FT	SIGNAL 1
FT	PROPEP 30
FT	CHAIN 33
FT	CHAIN 45
FT	PROPEP 323
FT	TRANSMEM 320
FT	DOMAIN 45
FT	DISULFID 37
FT	DISULFID 70
FT	DISULFID 168
FT	DISULFID 294
FT	PROTEIN 32
FT	PROSTATIN LIGHT CHAIN 44
FT	PROSTATIN HEAVY CHAIN 322
FT	POTENTIAL 343
FT	SERINE PROTEASE 286
FT	INTERCHAIN (BY SIMILARITY) 154
FT	BY SIMILARITY 86
FT	BY SIMILARITY 244

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC	NCBI_TaxID=9606;
CC	RN [1]
CC	RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
CC	RC TISSUE=Prostate;
CC	RX MEDLINE=9288644; PubMed=7768952;
CC	RA Yu J.X.; Chao L.; Chao J.J.;
CC	RT "Molecular cloning, tissue-specific expression, and cellular localization of human Prostasin mRNA.";
CC	RT J. Biol. Chem. 270:13483-13489(1995).
CC	RL J. Biol. Chem. 270:13483-13489(1995).
CC	RN [2]
CC	RP SEQUENCE FROM N.A.
CC	RC TISSUE=Placenta;
CC	RA Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC	RN [3]
CC	RP SEQUENCE OF 45-64.
CC	RC TISSUE=Semen;
CC	RX MEDLINE=94308140; PubMed=8034638;
CC	RA Yu J.X.; Chao L.; Chao J.J.;
CC	RT "Prostasin is a novel human serine proteinase from seminal fluid purification, tissue distribution, and localization in prostate gland.";
CC	RL J. Biol. Chem. 269:18843-18848(1994).
CC	-! FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY.
CC	-! SUBUNIT: HETERO-DIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULFIDE BOND.
CC	-! SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS.
CC	-! TISSUE SPECIFICITY: FOUND IN PROSTATE, LIVER, SALIVARY GLAND, KIDNEY, LUNG, PANCREAS, COLON, BRONCHUS AND RENAL PROXIMAL TUBULAR CELLS. IN THE PROSTATE GLAND IT MAY BE SYNTHESIZED IN EPITHELIAL CELLS, SECRETED INTO THE DUCTS, AND EXCRETED INTO THE SEMINAL FLUID.
CC	-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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CC	CC
CC	DR EMBL: L41351; AAC1759; 1; -.
CC	DR EMBL: U33446; AAB19071; 1; -.
CC	DR EMBL: BC001462; AAB101462; 1; -.
CC	DR HSSP: P00763; 1DPO.
CC	DR MEROPS: S01.159; 1.
CC	DR MMDB: 600823; -.
CC	DR InterPro: IPR001314; Chymotrypsin.
CC	DR InterPro: IPR001254; Trypsin.
CC	DR Pfam: PF00089; tryptsin; 1.
CC	DR PRANTS: PR00722; CHYMOTRYPSIN.
CC	DR SMART; SM0020; TRY_PSP; 1.
CC	DR PROSITE: PS05040; TRYPSIN_DOM; 1.
CC	DR PROSITE: PS00134; TRYPSIN_HIS; 1.
CC	DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; zymogen; Signal; Glycoprotein; Transmembrane.
FT	POTENTIAL 29
FT	ACTIVATION PEPTIDE 32
FT	PROSTATIN LIGHT CHAIN 44
FT	PROSTATIN HEAVY CHAIN 322
FT	POTENTIAL 343
FT	SERINE PROTEASE 286
FT	INTERCHAIN (BY SIMILARITY) 154
FT	BY SIMILARITY 86
FT	BY SIMILARITY 244

FT	DISULFID	201	223	BY SIMILARITY.
FT	DISULFID	234	262	BY SIMILARITY.
FT	ACT_SITE	85	85	CHARGE RELAY SYSTEM.
FT	ACT_SITE	134	134	CHARGE RELAY SYSTEM.
FT	CARBOHYD	238	238	CHARGE RELAY SYSTEM.
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	343 AA;	3643 AA;	MW: 98DD6447F5A8C1B2 CRC64;
Query Match		35.3%	Score 607.5; DB 1; Length 343;	POTENTIAL. PEPTIDE (BY SIMILARITY).
Best Local Similarity		44.2%	Pred. No. 2.9e-4; Matches 108; Indels 13; Gaps 7;	PROSTATIN LIGHT CHAIN.
Matches 129; Conservative		42;	Mismatches 108; Indels 13; Gaps 7;	PROSTATIN HEAVY CHAIN.
Qy	10 LGGGLGTFPSLL--LIASTAILNAARIAPVPPACGKPKQQLNRYVGGBSTDSEWPNTVS	66		POTENTIAL.
Db	7 LGPOLGAVAILLYGLRSGTGAEAAAP -- CGVAPAQ-A-RITGGSSAVAGQWPWQVS	61		SERINE PROTEASE.
Qy	67 IOKNGTHHCAGSLTTSRWTAAHCFKDNLNKPVLFSVILLGANOLGNPGRSQVKGVAWY	126		INTERCHAIN (BY SIMILARITY).
Db	62 ITYEGVHYGGSLVSEQWLVSAACFPSEHHE-AYEVKLAHQHOLDSYSEDAKVSTLRKI	120		BY SIMILARITY.
Qy	127 EPHPVYSWKEGACADIALYLERLTSIQFSERVLPICLIPDASITHLPPTNCTWISGWGSIODG	186		BY SIMILARITY.
Db	121 IHPSPY-LOGPSQCDIALLQLSREITSFSPYIRPCLPANAASPNGHCTVTGWGHAPS	179		BY SIMILARITY.
Qy	187 VPLPHQQTQKLKPYTIDSEVCSHLYWRCAGCOPP-ITDEMDLCAGYLEGERDAGLDGS	243		N-LINKED (GLCNAC. . .) (POTENTIAL).
Db	180 VSLLTPKPIQQLPEVPLISNETCNYNIDAKPPEPHYQEDWMCAGYEGGKDACQGDSG	239		POTENTIAL.
Qy	244 GPLMCOVDASWLLAGIISMGEGAAERNREGVYISSLSAHRSWKEVIVQGVQLR	295		BY SIMILARITY.
Db	240 GPLSCPVGEWLWLTGTIVSNGDACGARNPGVYTLOSSIASKVTELQPR	291		BY SIMILARITY.
RESULT	5			
PSS8_RAT				
ID	PSS8_RAT		STANDARD;	PRT;
AC	Q9E877; Q9ER01;			342 AA.
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Prostasin precursor (EC 3.4.21.-)			
GN	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NCBI_TaxID	10116;			
OX				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Adachi M.; Kitamura K.; Miyoshi T.; Tomita K.;			
RA	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Wang C.;			
RT	"Molecular cloning and expression of rat prostasin."			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
CC	-I - FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY SIMILARITY).			
CC	-I - SUBUNIT: HETERO-DIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULFIDE BOND (BY SIMILARITY).			
CC	-I - SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).			
CC	-I - SIMILARITY: BELONGS TO PEPTIDE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.			
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CC	RESULTS	6		
	TRYT_SHEEP		STANDARD;	RT;
ID	Q9ASM2;			273 AA.
AC	Q9ASM2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Tryptase 2 precursor (EC 3.4.21.59).			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.			
NCBI_TaxID	9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Abomasum.			
RA	Pemberton A.D., McAleese S.M., Huntley J.F., Mackellar A., Collie D.S., McMillan L., Scudamore C.L., Miller H.R.P.;			

"DNA sequence of sheep mast cell tryptase and its immunolocalisation in lung, skin and gut in comparison with sheep mast cell proteinase-1."
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DERANULATION RESPONSE OF THIS CELL TYPE.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
 CC -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. STRONGEST TO OTHER TRYPPTASES.

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CC EMBL: Y18224; CAB41989_1; -
 DR HSSP; P20231; IAA0.
 DR MEROPS; S01_143; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR PRNTS; PR00722; CHYMONTRYPSIN.
 DR SMART; SM00020; TRYSP_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
 CC SIGNAL PROPE 1 18 POTENTIAL.
 FT PROPE 19 28 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 29 273 TRYPTASE 2.
 FT ACT SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 222 222 BY SIMILARITY.
 FT DISULFID 153 73 BY SIMILARITY.
 FT DISULFID 157 228 BY SIMILARITY.
 FT DISULFID 186 209 BY SIMILARITY.
 FT CARBOHYD 218 246 BY SIMILARITY.
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 273 AA; 30288 MW; DE9BA7921BCE67D CRC64;

Query Match 33.6%; Score 578.5; DB 1; Length 273;
 Best Local Similarity 41.7%; Pred. No. 7.1e-43;
 Matches 115; Conservative 53; Mismatches 93; Indels 15; Gaps 7;

QY 21 LLLILASTAILNAAIRIPIPPACGKPQQLNRYVGGEDSTDSEMPWIVSIO---KNGTHHCAG 77
 Db 2 LHLIALLALSLSL-VSAAPAPGOALRSGIIGKEAPSRRNQVOSLVRDQYWRHQCGG 59

QY 78 SLLTSRWTIAACFKDNLNPKFLSVLGAQNPOSRSKQGVAVEPARYWSKEG 137
 Db 60 SLHPOWLTAAICIGPELQEPDSFRYQLEQHL---YYQDRLLPISRVIPPHYMYEN 116

QY 138 ACADIALYRLERLTSQFSRVLPICLPDASHLPPNTHCWSGWSIODGVPLPHPQTQLQK 197

Db 117 G-ADNLQLEPVLSHVQPTLPASETPPPESQWVTVGDVNGRPDPYPIKQ 175

QY 198 LKVPIIDSEVCSHLYWRGAGG---PIT-EDMCAGYLEGERDACLGDSGGPLMCOYDGA 253

Db 176 VKVPIVENSVCMDYHSGCAKPNRGPYIITRITSYLVCKVNT 289

QY 254 WLLAIGISWGEAERNPQGVISLSAHRSWKIV 289

Db 234 WLQAVVSWGDGCAKPNRGPYIITRITSYLVCKVNT 269

RESULT 7

PSS8_MOUSE

STANDARD:

PRP;

342 AA.

ID Q95SD1

AC DT

16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).

GN PRSS8 OR CAP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Vugniaux G.; Vallet V.; Fowler-Jaeger N.; Bens M.; Farman N.,

RA Courtois-Coutry N.; Vandewalle A.; Rossier B.C.; Hummler E.;

RT "Activation of the amiloride-sensitive sodium channel by the mouse serine protease mCaPi expressed in a principal kidney cell line."

RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RL CC -!- FUNCTION: POSSSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SODIUM CHANNELS.

CC -!- SUBUNIT: HETEROODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULFIDE BOND (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 339.

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CC DR EMBL: AP188613; AAC170454.1; ALT_FRAME.

CC DR InterPro: IPRE001254; Trypsin.

CC PFAM: PF00089; Trypsin; 1.

CC SMART: SM00030; TRYSP_SPC; 1.

CC PROSITE: PS50240; TRYPSIN_DOM; 1.

CC DR PROSITE: PS00134; TRYPSIN_HIS; 1.

CC DR PROSITE: PS00135; TRYPSIN_SER; 1.

CC DR PROSITE: PS00136; TRYPSIN_NH2; 1.

CC DR PROSITE: PS00137; TRYPSIN_NH3; 1.

CC DR PROSITE: PS00138; TRYPSIN_NH4; 1.

CC DR PROSITE: PS00139; TRYPSIN_NH5; 1.

CC DR PROSITE: PS00140; TRYPSIN_NH6; 1.

CC DR PROSITE: PS00141; TRYPSIN_NH7; 1.

CC DR PROSITE: PS00142; TRYPSIN_NH8; 1.

CC DR PROSITE: PS00143; TRYPSIN_NH9; 1.

CC DR PROSITE: PS00144; TRYPSIN_NH10; 1.

CC DR PROSITE: PS00145; TRYPSIN_NH11; 1.

CC DR PROSITE: PS00146; TRYPSIN_NH12; 1.

CC DR PROSITE: PS00147; TRYPSIN_NH13; 1.

CC DR PROSITE: PS00148; TRYPSIN_NH14; 1.

CC DR PROSITE: PS00149; TRYPSIN_NH15; 1.

CC DR PROSITE: PS00150; TRYPSIN_NH16; 1.

CC DR PROSITE: PS00151; TRYPSIN_NH17; 1.

CC DR PROSITE: PS00152; TRYPSIN_NH18; 1.

CC DR PROSITE: PS00153; TRYPSIN_NH19; 1.

CC DR PROSITE: PS00154; TRYPSIN_NH20; 1.

CC DR PROSITE: PS00155; TRYPSIN_NH21; 1.

CC DR PROSITE: PS00156; TRYPSIN_NH22; 1.

CC DR PROSITE: PS00157; TRYPSIN_NH23; 1.

CC DR PROSITE: PS00158; TRYPSIN_NH24; 1.

CC DR PROSITE: PS00159; TRYPSIN_NH25; 1.

CC DR PROSITE: PS00160; TRYPSIN_NH26; 1.

CC DR PROSITE: PS00161; TRYPSIN_NH27; 1.

CC DR PROSITE: PS00162; TRYPSIN_NH28; 1.

CC DR PROSITE: PS00163; TRYPSIN_NH29; 1.

CC DR PROSITE: PS00164; TRYPSIN_NH30; 1.

CC DR PROSITE: PS00165; TRYPSIN_NH31; 1.

CC DR PROSITE: PS00166; TRYPSIN_NH32; 1.

CC DR PROSITE: PS00167; TRYPSIN_NH33; 1.

CC DR PROSITE: PS00168; TRYPSIN_NH34; 1.

CC DR PROSITE: PS00169; TRYPSIN_NH35; 1.

CC DR PROSITE: PS00170; TRYPSIN_NH36; 1.

CC DR PROSITE: PS00171; TRYPSIN_NH37; 1.

CC DR PROSITE: PS00172; TRYPSIN_NH38; 1.

CC DR PROSITE: PS00173; TRYPSIN_NH39; 1.

CC DR PROSITE: PS00174; TRYPSIN_NH40; 1.

CC DR PROSITE: PS00175; TRYPSIN_NH41; 1.

CC DR PROSITE: PS00176; TRYPSIN_NH42; 1.

CC DR PROSITE: PS00177; TRYPSIN_NH43; 1.

CC DR PROSITE: PS00178; TRYPSIN_NH44; 1.

CC DR PROSITE: PS00179; TRYPSIN_NH45; 1.

CC DR PROSITE: PS00180; TRYPSIN_NH46; 1.

CC DR PROSITE: PS00181; TRYPSIN_NH47; 1.

CC DR PROSITE: PS00182; TRYPSIN_NH48; 1.

CC DR PROSITE: PS00183; TRYPSIN_NH49; 1.

CC DR PROSITE: PS00184; TRYPSIN_NH50; 1.

CC DR PROSITE: PS00185; TRYPSIN_NH51; 1.

CC DR PROSITE: PS00186; TRYPSIN_NH52; 1.

CC DR PROSITE: PS00187; TRYPSIN_NH53; 1.

CC DR PROSITE: PS00188; TRYPSIN_NH54; 1.

CC DR PROSITE: PS00189; TRYPSIN_NH55; 1.

CC DR PROSITE: PS00190; TRYPSIN_NH56; 1.

CC DR PROSITE: PS00191; TRYPSIN_NH57; 1.

CC DR PROSITE: PS00192; TRYPSIN_NH58; 1.

CC DR PROSITE: PS00193; TRYPSIN_NH59; 1.

CC DR PROSITE: PS00194; TRYPSIN_NH60; 1.

CC DR PROSITE: PS00195; TRYPSIN_NH61; 1.

CC DR PROSITE: PS00196; TRYPSIN_NH62; 1.

CC DR PROSITE: PS00197; TRYPSIN_NH63; 1.

CC DR PROSITE: PS00198; TRYPSIN_NH64; 1.

CC DR PROSITE: PS00199; TRYPSIN_NH65; 1.

CC DR PROSITE: PS00200; TRYPSIN_NH66; 1.

CC DR PROSITE: PS00201; TRYPSIN_NH67; 1.

CC DR PROSITE: PS00202; TRYPSIN_NH68; 1.

CC DR PROSITE: PS00203; TRYPSIN_NH69; 1.

CC DR PROSITE: PS00204; TRYPSIN_NH70; 1.

CC DR PROSITE: PS00205; TRYPSIN_NH71; 1.

CC DR PROSITE: PS00206; TRYPSIN_NH72; 1.

CC DR PROSITE: PS00207; TRYPSIN_NH73; 1.

CC DR PROSITE: PS00208; TRYPSIN_NH74; 1.

CC DR PROSITE: PS00209; TRYPSIN_NH75; 1.

CC DR PROSITE: PS00210; TRYPSIN_NH76; 1.

CC DR PROSITE: PS00211; TRYPSIN_NH77; 1.

CC DR PROSITE: PS00212; TRYPSIN_NH78; 1.

CC DR PROSITE: PS00213; TRYPSIN_NH79; 1.

CC DR PROSITE: PS00214; TRYPSIN_NH80; 1.

CC DR PROSITE: PS00215; TRYPSIN_NH81; 1.

CC DR PROSITE: PS00216; TRYPSIN_NH82; 1.

CC DR PROSITE: PS00217; TRYPSIN_NH83; 1.

CC DR PROSITE: PS00218; TRYPSIN_NH84; 1.

CC DR PROSITE: PS00219; TRYPSIN_NH85; 1.

CC DR PROSITE: PS00220; TRYPSIN_NH86; 1.

CC DR PROSITE: PS00221; TRYPSIN_NH87; 1.

CC DR PROSITE: PS00222; TRYPSIN_NH88; 1.

CC DR PROSITE: PS00223; TRYPSIN_NH89; 1.

CC DR PROSITE: PS00224; TRYPSIN_NH90; 1.

CC DR PROSITE: PS00225; TRYPSIN_NH91; 1.

CC DR PROSITE: PS00226; TRYPSIN_NH92; 1.

CC DR PROSITE: PS00227; TRYPSIN_NH93; 1.

CC DR PROSITE: PS00228; TRYPSIN_NH94; 1.

CC DR PROSITE: PS00229; TRYPSIN_NH95; 1.

CC DR PROSITE: PS00230; TRYPSIN_NH96; 1.

CC DR PROSITE: PS00231; TRYPSIN_NH97; 1.

CC DR PROSITE: PS00232; TRYPSIN_NH98; 1.

CC DR PROSITE: PS00233; TRYPSIN_NH99; 1.

CC DR PROSITE: PS00234; TRYPSIN_NH100; 1.

CC DR PROSITE: PS00235; TRYPSIN_NH101; 1.

CC DR PROSITE: PS00236; TRYPSIN_NH102; 1.

CC DR PROSITE: PS00237; TRYPSIN_NH103; 1.

CC DR PROSITE: PS00238; TRYPSIN_NH104; 1.

CC DR PROSITE: PS00239; TRYPSIN_NH105; 1.

CC DR PROSITE: PS00240; TRYPSIN_NH106; 1.

CC DR PROSITE: PS00241; TRYPSIN_NH107; 1.

CC DR PROSITE: PS00242; TRYPSIN_NH108; 1.

CC DR PROSITE: PS00243; TRYPSIN_NH109; 1.

CC DR PROSITE: PS00244; TRYPSIN_NH110; 1.

CC DR PROSITE: PS00245; TRYPSIN_NH111; 1.

CC DR PROSITE: PS00246; TRYPSIN_NH112; 1.

CC DR PROSITE: PS00247; TRYPSIN_NH113; 1.

CC DR PROSITE: PS00248; TRYPSIN_NH114; 1.

CC DR PROSITE: PS00249; TRYPSIN_NH115; 1.

CC DR PROSITE: PS00250; TRYPSIN_NH116; 1.

CC DR PROSITE: PS00251; TRYPSIN_NH117; 1.

CC DR PROSITE: PS00252; TRYPSIN_NH118; 1.

CC DR PROSITE: PS00253; TRYPSIN_NH119; 1.

CC DR PROSITE: PS00254; TRYPSIN_NH120; 1.

CC DR PROSITE: PS00255; TRYPSIN_NH121; 1.

CC DR PROSITE: PS00256; TRYPSIN_NH122; 1.

CC DR PROSITE: PS00257; TRYPSIN_NH123; 1.

CC DR PROSITE: PS00258; TRYPSIN_NH124; 1.

CC DR PROSITE: PS00259; TRYPSIN_NH125; 1.

CC DR PROSITE: PS00260; TRYPSIN_NH126; 1.

CC DR PROSITE: PS00261; TRYPSIN_NH127; 1.

CC DR PROSITE: PS00262; TRYPSIN_NH128; 1.

CC DR PROSITE: PS00263; TRYPSIN_NH129; 1.

CC DR PROSITE: PS00264; TRYPSIN_NH130; 1.

CC DR PROSITE: PS00265; TRYPSIN_NH131; 1.

CC DR PROSITE: PS00266; TRYPSIN_NH132; 1.

CC DR PROSITE: PS00267; TRYPSIN_NH133; 1.

CC DR PROSITE: PS00268; TRYPSIN_NH134; 1.

CC DR PROSITE: PS00269; TRYPSIN_NH135; 1.

CC DR PROSITE: PS00270; TRYPSIN_NH136; 1.

CC DR PROSITE: PS00271; TRYPSIN_NH137; 1.

CC DR PROSITE: PS00272; TRYPSIN_NH138; 1.

CC DR PROSITE: PS00273; TRYPSIN_NH139; 1.

CC DR PROSITE: PS00274; TRYPSIN_NH140; 1.

CC DR PROSITE: PS00275; TRYPSIN_NH141; 1.

CC DR PROSITE: PS00276; TRYPSIN_NH142; 1.

CC DR PROSITE: PS00277; TRYPSIN_NH143; 1.

CC DR PROSITE: PS00278; TRYPSIN_NH144; 1.

CC DR PROSITE: PS00279; TRYPSIN_NH145; 1.

CC DR PROSITE: PS00280; TRYPSIN_NH146; 1.

CC DR PROSITE: PS00281; TRYPSIN_NH147; 1.

CC DR PROSITE: PS00282; TRYPSIN_NH148; 1.

CC DR PROSITE: PS00283; TRYPSIN_NH149; 1.

Db	7	LGLGOLEAVTILLLG-LIQLSIRADGTASCGAVIQ-PRITGGGSAKPQGWQVQSLT	63
Qy	69	KNGTHHCAGSLTTSKVVITAHCFC-KDNLHKPYLFESVLIGAQLGNGPSISQKVGAWE	127
Db	64	YDGHNIVCGGSEVSNKWVSSAHCFPREHSEAY-EVKLGAAHQLDYSNTDVVHTVAQII	121
Qy	128	PHPVYSWKEGACADIALVRILERSOFPLCIPDASHLPPNTHCMTSQNGSIODGV	187
Db	122	THSSYR-EEGSQGDAFIRLSPPTFSRYTRICPAUNASFPGLHCTVGMQHVAPESV	1.
Qy	188	PLPHPHOTLQKLVKUPTIDSECSHLY-WRGAGQGP-ITEDMLCAGYLEGERDACLGDSCG	244
Db	181	SLQTTPRLPQLEVPISRETCSCLYNNINAVPEEPHTIQDMCLCAGYVGKDKACQGDSCG	240
Qy	245	PLMCQVDGAWMALLAGTISWGCAEENRPGVYISLSAHRSWEKTVQGYOLR	295
Db	241	PLSCPMEGIWLAGTISWGCAEENRPGVYISLSAHRSWEKTVQGYOLR	291
RESULT 8			
ID	TRYG_HUMAN	STANDARD; PRT;	321 AA.
AC	Q9NRB2; Q9NC015; Q9NRQ6;	PRT; Q9NRQ6; Q9NC015; Q9NRB2;	
DT	16-Oct-2001 (Rel. 40, Created)		
DT	16-Oct-2001 (Rel. 40, Last annotation update)		
DT	16-Oct-2001 (Rel. 40, Last annotation update)		
DE	tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).		
GN	TGSG1 OR TMT.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID	9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).		
RX	MEDLINE=20302813; PubMed=10843716;		
RA	Caughey G.H.; Raymond W.W.; Blount J.L.; Hau L.W.; Pallaoro M.,		
RA	Wolters P.J.; Verghese G.M.;		
RT	"Characterization of human gamma-trypases, novel members of the chromosome 16p mast cell tryptase and prostanin gene families."		
RT	J. Immunol. 165:6566-6575(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94452974; PubMed=10521469;		
RA	Wong G.W.; Tang Y.; Feyant E.; Sali A.; Li L.; Li Y.; Huang C.,		
RA	Friend D.S.; Krilis S.A.; Stevens R.L.;		
RT	"Identification of new member of the trypase family of mouse and human mast cell proteases which possesses a novel COOH-terminal hydrophobic extension."		
RL	J. Biol. Chem. 274:30784-30793(1999).		
RN	[3]		
RP	SEQUENCE OF 220-321 FROM N.A.		
RA	Mitterer S., Agnew W.S.;		
RT	"Organization and alternative splicing of CACNA1H."		
RL	Subunits (JAN-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1 SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).		
CC	-1 TISSUE SPECIFICITY: Expressed in many tissues.		
CC	-1 POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues.		
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY 31; ALSO KNOWN AS THE TRYPTASE SUBFAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	DR: AP191031; ARF76457.1; .		
DR	EMBL: AF195508; AAF76458.1; .		
DR	EMBL: AF175759; AAF03697.1; .		
DR	EMBL: AF175522; AAF03695.1; .		
RESULT 9			
ID	MCP76_MOUSE	STANDARD;	PRT; 276 AA.
AC	P21845; 061362;		
DT	01-MAY-1991 (Rel. 18, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Mast cell protease 6 precursor (EC 3.4.21.59) (MMCP-6) (tryptase).		
GN	MCP76.		

OS Mus musculus (Mouse). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91139602; PubMed=11995638;
 RX REYNOLDS D.S., GURLEY D.S., AUSTEN K.F., SERAFIN W.E.;
 RA "Cloning of the cDNA and gene of mouse mast cell protease-6."
 RT "Transcription by promoter mast cells and mast cells of the
 connective tissue subclass.";
 RT J. Biol. Chem. 266:3847-3853(1991).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=LEIDEN X AL;
 RC MEDLINE=94023807; PubMed=8210998;
 RA Huang R., Abrink M., Gobl A.E., Nilsson G., Avestogh M., Larsson L.G.,
 RA Nilsson K., Hellman L.;
 RT "Expression of a mast cell tryptase in the human monocytic cell lines
 U-937 and Mono Mac 6.;"
 RT Scand. J. Immunol. 38:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC STRAIN=LEIDEN X AL;
 RX MEDLINE=93048552; PubMed=7959952;
 RA Huang R., Hellman L.T.;
 RT "Genes for mast-cell serine protease and their molecular evolution."
 RL Immunogenetics 40:397-414(1994).
 RN [4]
 RP SEQUENCE OF 32-54.
 RX MEDLINE=9022202; PubMed=2326280;
 RA REYNOLDS D.S., STEVENS R.L., LANE W.S., CARR M.H., AUSTEN K.F.,
 RA SERAFIN W.E.;
 RA "Different mouse mast cell populations express various combinations
 of at least six distinct mast cell serine proteases.";
 RP Proc. Natl. Acad. Sci. U S A. 87:3230-3234(1990).
 -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 RESPONSE OF THIS CELL TYPE.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -!- ALTERNATIVE PRODUCTS: TWO FORMS OF MCPT6 ARE PRODUCED BY
 CC A NON FUNCTIONAL VARIANT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY TRYPTASE SUBFAMILY.

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CC EMBL; M57626; AAQ39888_1; -;
 DR EMBL; M57625; AAQ39887_1; -;
 DR EMBL; L31853; AAQ39725_1; -;
 DR EMBL; X78542; CAA55388_1; -;
 PIR; A38654; A38654;
 PIR; D35646; D35646;
 HSSP; P20231; IAO0;
 MEROP; SOL0025; -;
 DR MGD; MGI:166942; MCPT6;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHMOTRIPSIN.
 DR SMART; SM00020; TRYP_SPC_1.
 DR PROSITE; PS50240; TRYPSIN_DOMAIN_1.
 DR PROSITE; PS00134; TRYPSIN_HIS_1.
 DR PROSITE; PS00135; TRYPSIN_SER_1.
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;

KW Alternative splicing. 21
 FT SIGNAL 1 31
 FT PROPEP 22 31
 FT CHAIN 32 276
 FT ACT_SITE 75 75
 FT ACT_SITE 122 122
 FT ACT_SITE 225 225
 FT DISULFID 60 76
 FT DISULFID 156 231
 FT DISULFID 189 212
 FT DISULFID 221 249
 FT CARBOHYD 133 133
 FT VARSPUIC 223 230
 FT VARSPUIC 231 276
 SQ SEQUENCE 276 AA; MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 276 AA; 30927 MW; 525522C9A04A72200 CRC64;

Query Match 32.2%; Score 554; DB 1; Length 276;
 Best Local Similarity 41.6%; Pred. No. 9.4e-11;
 Matches 116; Conservative 48; Mismatches 93; Indels 22; Gaps 9;

Qy 21 LLILLASITNAARIPPV-PAGKREQQQLNLKPYLFSVLLGAWQL-GNPGSRSSQKVGVAVWEPHPVYSW 134
 Db 6 LLLFLALSLASLVLVYSAAPRRA---NQRYIVGHEASESEKWKPVQVSLSRFPKLYNWIHFCC 61
 Qy 77 GSLLTSRWRVITAACFKDNLNKPYLFSVLLGAWQL-GNPGSRSSQKVGVAVWEPHPVYSW 134
 Db 62 GSLIHPQWVITAACVGPHIKSPQFLVRQIREQQIYGD----OILSLRIVWPHYGD----OILSLRIVWPHYGD 116
 Qy 135 KEGACADIALVRLERSIQFSERVLPCIPDASHIPLPPNTCHWISGWGSIODGVPLPHPQT 194
 Db 117 AEGG-ADVALLEPVEPVNTSHIPTSLPPEAEPPGTSWCWIGDWIDNEPLPPVPP 175
 Qy 195 LOKLKVPITDSEVCSHLVYNGAGQG--PITED-MUCAGLEDEGDDGSGGPIMCVO 250
 Db 176 LKQVKVPITVENSLSLCDRKYHTGLYTDGDFPVHDGMCLAG--NTRRDSCQGDSGGPLVCKV 233
 Qy 251 DGAWILLAGLIIISWEGCAERNRPGVYTSLSAHRSYWEKIV 289
 Db 234 KGFTWLQAGVVSWEGCAQPNNKGITTRYTYLDWTHRYV 272
 RESULT 10
 TRYT_CANFA ID TRYT_CANFA STANDARD; PRT; 275 AA.
 AC P15944;
 AC 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 - DE Trypsine precursor (EC 3.4.21.59).
 - OS Canis familiaris (Dog).
 CC FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -!- ALTERNATIVE PRODUCTS: TWO FORMS OF MCPT6 ARE PRODUCED BY
 CC A NON FUNCTIONAL VARIANT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY TRYPTASE SUBFAMILY.

SEQUENCE FROM N.A.
 RX MEDLINE=83352460; PubMed=2504277;
 RA Vandervlice P., Craik C.S., Nadel J.A., Caughey G.H.,
 RA "Molecular cloning of dog mast cell tryptase and a related protease:
 RT structural evidence of a unique mode of serine protease activation.";
 RL Biochemistry 28:4148-4155(1989).
 -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -!- SUBUNIT: HOMOTRIMER.
 CC -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 CC MAST CELL ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. STRONGEST TO OTHER TRYPTASES.
 CC ---

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CC SEQUENCE FROM N.A.
 CC TISSUE=Peritoneal mast cells;
 CC MEDLINE=96015171; PubMed=8537314;
 CC RA Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
 CC RA Maruyama H., Osada Y., Nawa Y.;
 CC RT cDNA sequencing and expression of rat mast cell tryptase.;"
 CC J. Biochem. 118:210-215(1995).
 DR [12].
 DR RN
 DR SEQUENCE FROM N.A.
 DR RP STRAIN=SPPAGUE-DAWLEY; TISSUE=Peritoneal mast cells;
 DR RC RX MEDLINE=97149430; PubMed=8996338;
 DR RA Lutzelschwab C., Peijer G., Averskog M., Hellman L.;
 DR RT "Secretory granule proteases in rat mast cells. Cloning of 10 different serine proteases and a carboxypeptidase A from various rat mast cell populations."
 DR RT J. Exp. Med. 185:13-29 (1997).
 DR RT !- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS, AND IS RETAINED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.
 DR RT !- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-, Lys-1-, but with more restricted specificity than trypsin.
 DR RT !- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. STRONGEST TO OTHER TRYPISES.
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 DR RT !- EMBL: D3B8455; BAA07486_1; -.
 DR DR EMBL: U67509; AAB48262_1; -.
 DR DR HSSP, P20231; 1AA0.
 DR DR MEROPS; S01_025; -.
 DR DR InterPro; IPR001314; Chymotrypsin.
 DR DR InterPro; IPR001254; Trypsin.
 DR DR Pfam; PF0089; trypsin; 1.
 DR DR SMART; PRO0072; CHYMOTRYPTIN.
 DR DR PROSITE; PS00020; TRYP_SPC_1.
 DR DR PROSITE; PS00134; TRYPSIN_DOM.
 DR DR PROSITE; PS00135; TRYPSIN_HIS.
 DR DR PROSITE; PS00135; TRYPSIN_SER.
 DR DR Hydrolase; Serine protease; Glycoprotein; Zymogen.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 31 275 TRYPSINE.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISUFID 59 75 BY SIMILARITY.
 FT DISUFID 155 230 BY SIMILARITY.
 FT DISUFID 188 211 BY SIMILARITY.
 FT DISUFID 220 248 BY SIMILARITY.
 FT CARBOHYD 132 132 N-LINED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 275 AA; C3B86925|F248D5B CRC64;

Query Match 31.7%; Score 546; DB 1; Length 275;
 Best Local Similarity 40.9%; Pred. No. 4.6e-40;
 Matches 112; Conservative 46; Mismatches 102; Indels 14; Gaps 6;

Qy 23 LLASTAILNARIPVPPACKPQQLNRRVGGEDSTDSEMPWIVSIQKNS---THHCAGSL 79
 Db 5 LVLAIALLGSL-VPVSPPAQALQRGVITGVGREAPGSKWPQYSLRLKGQYWRHICGSSL 63
 Qy 80 LTSRQVITAHCFKDNLNKPYLEFSVLLGAWLGNPGSRSQKVGYAWVEPHYPSWKEGAC 139
 Db 64 IHPQWVLTAAHCVGPNVCEBEIRVQLREOHL---YYQDHLLPVNRVTPHNPVTPENS- 119
 Qy 140 ADIALYRLERSTIQFSEVLPICLPDASIHLPPLGDYPLPHPOTLQKLK 199
 Db 120 ADIALELEDPVNSAHQVTLPALQTFPTGTPCWTGWDVHSGTPLPPFPFLPKVK 179
 Qy 200 VPIDSEVCSHLYARGAGQGP---ITEMLCAGYLEGRDACLGDSGCPMLQVQDGAML 255
 Db 180 VPIVENSMCQYQHIGLSDGVTRDEMILCAG--NSRSKDSQQGSDGSPLVCRVRGVWL 237
 Qy 256 LAGTISWGECAERNRPGTYTISLSAHRSWEKETV 289
 Db 238 QAGVIVSWGECAQPNNRPGIYTRVAYLDMHQYV 271
 RESULT 11
 ID MCT6_RAT STANDARD; PRT; 274 AA.
 AC P50343; P97593;
 AC DT 01-Oct-1996 (Rel. 34, Created)
 AC DT 01-Oct-1996 (Rel. 34, Last sequence update)
 AC DT 16-Oct-2001 (Rel. 40, Last annotation update)
 AC Mast cell protease 6 precursor (EC 3.4.21.59) (RMCP-6) (Tryptase).
 GN MCP6 OR MCP6.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116;
 RN [1]

Query Match 31.3%; Score 538.5; DB 1; Length 274;
 Best Local Similarity 40.6%; Pred. No. 2e-39;
 Matches 117; Conservative 46; Mismatches 84; Indels 41; Gaps 10;

Qy 21 LLILAST---AIIINAARIIPVPPACGKPKQQLNRYGGEDSTDSEMPWIVSIQKNGT---HH 74
 Db 5 LLILALSPASLYHAAPCPVKQRYV----IVGGREASESFWPMQVSLRFKFSFWNHF 57
 Qy 75 CAGSLLTSEWVITAHCFKDNLNKPYLEFSVLLGAWLGNPGSRQ-----KGVAV 125

Db	58	CGGSLTHPQWVLTAAVGVLHKSPELFROYL-----REQLYYADQLLTVNRTV	107		FT DISULFID 155 230 BY SIMILARITY.	
QY	126	VEPHPVISWKEACADIALVRLERSTQFSERVLPICUPDASTHLPPNTHCNISGNQSIQD	185		FT DISULFID 188 211 BY SIMILARITY.	
Db	108	VPHF-YTVVEDG-ADFALEELIP/NVSTHHPISUPPASETFPSGTSCWVTCGWCDIDS	164		FT DISULFID 220 248 BY SIMILARITY.	
QY	186	GVPFLPHPTOLQKTPIDSEVCYSHLYWRGAGQ--PITED-MUCAGYLEGERDACLGD	241		FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).	
Db	165	DEPLLPYPLKVKPVIVENSLDKRYHTGLTYGDDYPIVQDGMLCAG-NTRSDSCQGD	222		FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).	
QY	242	SGGPLMCOVDGAWLLAGIISNGEGCAERNRPGVYISUSAHSRWSVEKIV	289		SQ SEQUENCE 275 AA; 30439 MW; ACC5B2647FCCB973 CRC64;	
Db	223	SGPLVCKVKGMWLAQEVNSNGECAEAANRPQIYTRVTTYLDWIHYV	270			
RESULT 12						
TRYT_PIG	ID TRYT_PIG	STANDARD;	PRT;	275 AA.	Query Match 31.0%; Score 532.5; DB 1; Length 275;	
AC QPN1D1;	AC QPN1D1;				Best Local Similarity 39.4%; Pred. No. 6.7e-39;	
DT 16-OCT-2001 (Rel. 40, Created)					Matches 109; Conservative 53; Mismatches 100; Indels 15; Gaps 7;	
DR 16-OCT-2001 (Rel. 40, Last sequence update)						
DT 16-OCT-2001 (Rel. 40, Last annotation update)						
DE TRYptase precursor (EC 3.4.21.59). MCT7.						
GN OS						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suisidae; Sus.						
CA RCB1_TAXID=9823;						
RN [1]						
RP SEQUENCE FROM N.A.						
RC TISSUE=Lung;						
RA Chen Y., Shioota M., Ohuchi M., Towatari T., Tashiro J., Murakami M., Yano M., Yang B., Kido H.; RT A novel trypsin-type protease from pig lungs, triggering infection by pneumotropic viruses: purification and characterization. ";					RESULT 13	
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.					TEST_HUMAN	
CC -1- FUNCTION: TRYPtase IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION					ID TEST_HUMAN STANDARD; PRT; 314 AA.	
CC -1- REACTIONS OF THIS CELL TYPE.					AC Q9Y6M0; Q9N341; Q9P2V6;	
CC -1- CARBLYtic ACTIVITY: Preferential cleavage: Arg- -, Lys- -, but with more restricted specificity than trypsin.					DT 16-OCT-2001 (Rel. 40, Created)	
CC -1- SUBUNIT: HOMOTETRAMER (By similarity).					DT 16-OCT-2001 (Rel. 40, Last sequence update)	
CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.					DT 16-OCT-2001 (Rel. 40, Last annotation update)	
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPtIN FAMILY. STRONGEST TO OTHER TRYPtASES.					DE Testisin precursor (EC 3.4.21.-) (Eosinophil serine protease 1) (ESP-1).	
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CC -1- EMBL: AB038652; BAA93614.1; -.					GN Homo sapiens (Human).	
CC -1- MEROPS: S01.143; -.					OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. NCBI_TaxID=9606;	
CC -1- DR InterPro: IPR001314; Chymotrypsin.					RN [1]	
CC -1- DR InterPro: IPR001554; Trypsin.					RN Sequence FROM N.A. (ISOFORM 1).	
CC -1- DR Pfam: PF00089; trypsin; 1.					RC ISOFORM 1.	
CC -1- DR PRINTS: PR00722; CHYMOTRYPSIN.					RC TISSUE=Eosinophil; MEDLINE=99045401; PubMed=9826525;	
CC -1- DR SMART: SM00020; TRY_SPc; 1.					RC Inoue M., Isobe M., Itoyama T., Kido H.; RA "Cloning and tissue distribution of a novel serine protease esp-1 from human eosinophils"; RL BiChem. Biophys. Res. Commun. 266:564-568(1999).	
CC -1- DR PROSITE: PS050240; TRYPSIN_DOM; 1.					RN [3]	
CC -1- DR PROSITE: PS00134; TRYPSIN_HIS; 1.					RN Sequence FROM N.A. (ISOFORMS 1 AND 2).	
CC -1- DR PROSITE: PS00135; TRYPSIN_SER; 1.					RC TISSUE=Cervical carcinoma; RX MEDLINE=20058805; PubMed=1060542;	
CC -1- KW Hydrolase; Serine protease; Glycoprotein; Zymogen.					RA Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L., RA Normyle J.F., Stuttard M.A., Douglas M.L., Loveland K.A., RA "Structural analysis of esp-1 gene (PRSS 21)." RT "testisin, a new human serine proteinase expressed by premeiotic testicular germ cells and lost in testicular germ cell tumors." RT Cancer Res. 59:3199-3205(1999).	
FT SIGNAL 1 20 POTENTIAL.					RL Cancer Res. 59:3199-3205(1999).	
FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).					RN [4]	
FT CHAIN 31 275 TRYPTASE.					RP SEQUENCE FROM N.A.	
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).					RC MEDLINE=99323395; PubMed=10397266;	
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).					RA Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L., RA Normyle J.F., Stuttard M.A., Douglas M.L., Loveland K.A., RA "Structural analysis of esp-1 gene (PRSS 21)." RT "testisin, a new human serine proteinase expressed by premeiotic testicular germ cells and lost in testicular germ cell tumors." RT Cancer Res. 59:3199-3205(1999).	
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).					RP SEQUENCE FROM N.A.	
FT DISULFID 75 75 BY SIMILARITY.						

RA Matschner G., Fritz H., Sommerhoff C.P., Bode W.;
 RT "Human beta-trypsinase is a ring-like tetramer with active sites facing
 a central pore.";
 RT Nature 392:306-311(1998).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RX MEDINE=9432168; PubMed=10500112;
 RA Sommerhoff C.P., Bode W., Pereira P.J.B., Stubbs M.T.,
 RA Stuerzebecher J., Piechottka G.P., Matschner G., Bergner A.;
 RT "the structure of the human beta1-trypsinase tetramer: four better or
 worse";
 Proc. Natl. Acad. Sci. U.S.A. 96:10984-10991(1999).
 RL - FUNCTION: TRYPSINASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 RESPONSE OF THIS CELL TYPE.
 CC - CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-| -, but
 CC with more restricted specificity than trypsin.
 CC - SUBUNIT: HOMOTETRAMER.
 CC - SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 MAST CELL ACTIVATION.
 CC - POLYMORPHISM: There are two alleles; beta-II and beta-III which
 differ by 3 residues.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. TRYPTASE SUBFAMILY.

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DR EMBL; M37488; AAA51843.1;
 DR EMBL; M33492; AAA36779.1;
 DR EMBL; M33493; AAA36780.1;
 DR EMBL; M33551; AAA36781.1;
 DR EMBL; AF099143; AACDI3876.1;
 DR EMBL; AF099145; AACDI7857.1;
 DR EMBL; AF099146; AACDI7858.1;
 DR PIR; A37193; A37193;
 DR PF0089; PF0089; trypsin.1;
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 SMART; SM00020; TRY_PSPC_1.
 PROSITE; PS00240; TRYPSIN_DOM; 1;
 PROSITE; PS00134; TRYPSIN_HIS; 1;
 PROSITE; PS00135; TRYPSIN_SER; 1;
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
 KW Polymorphism; 3D-structure.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 30 ACTIVATION PEPTIDE.
 FT CHAIN 31 275 TRYPTASE BETA-2.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM.
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT DISULFID 59 75
 FT DISULFID 155 230
 FT DISULFID 188 211
 FT DISULFID 220 248
 FT CARBOHYD 233 233 N-LINKED (GLCNAC-⁻) (POTENTIAL).
 FT VARIANT 51 53 HGP -> RDR (IN BETA-III).
 /FT id=VAR_012:04.
 FT CONFLICT 132 132 K -> N (IN REF 3).
 SQ SEQUENCE 275 AA; 30529 MW; 2B27396C51F5C7A0 CRC64;

	Best Local Similarity 39.2%; Pred. No. 1e-38;
	Matches 113; Conservative 53; Mismatches 85; Indels 37; Gaps 9;
Qy	20 SLILLASATILNARIPPPACGRQQNRRGGEDSTDSEWIVSQKNG--THICA 76
Db	3 NLLILAPVL-A-ASRAYAAPGSGALQRNGTIVGGQEADRSKWPVQSRVHPYMMHPCG 60
Qy	77 GSLLTSRVVTAHC---FKD----NLNKPLFSTYLLGARQLGNPGSRQKVGVWW 126
Db	61 GSLIHPQWLAATHCVCGDVKDIAALRQLREOHY-----YDQDLPVRI 107
Qy	127 EPHP-VYNSKEGACADILVLRLRSIQSERVPLCLPDDASHLPPNTCHWISGWGS1QD 185
Db	108 IVHPIQFYTAQIG-ADIALLELEPVKTVSHVHTVLPASETFPPGAPCWWTRGWDVDN 165
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -, Lys- -, but CC with more restricted specificity than trypsin.	CC -1- CATALYTIC ACTIVITY: CLEAGLEGENDACIJD 241
CC -1- SUBUNIT: HOMOTETRAMER.	CC -1- DEDMLCAGLLEGENDACIJD 241
CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON	CC -1- DEDMLCAGLLEGENDACIJD 241
CC -1- MAST CELL ACTIVATION.	CC -1- DEDMLCAGLLEGENDACIJD 241
CC -1- POLYMORPHISM: There are two alleles; beta-II and beta-III which	CC -1- DEDMLCAGLLEGENDACIJD 241
CC -1- differ by 3 residues.	CC -1- DEDMLCAGLLEGENDACIJD 241
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE	CC -1- DEDMLCAGLLEGENDACIJD 241
CC TRYPTASE SUBFAMILY.	CC -1- DEDMLCAGLLEGENDACIJD 241
	RESULT 15
	TEST_MOUSE STANDARD; PRT; PRT;
ID	TEST_MOUSE STANDARD;
AC	Q9AII7; Q9DA14;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Testisin precursor (EC 3.4.21.-) (tryptase 4).
GN	PRSS21.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID	10909;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129/SV;
RX	Medline=21153229; PubMed=11231276;
RA	Scarman A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C.,
RA	Nonnyle J.F., Antalis T.M.;
RT	"Organization and chromosomal localization of the murine Testisin gene encoding a serine protease temporally expressed during spermatogenesis.";
RT	Eur. J. Biochem. 268:1250-1258 (2001).
RL	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C; TISSUE=Testis;
RX	Medline=1125947;
RA	Wong G.W., Li L., Madhusudhan M.S., Kritis S.A., Gurish M.F.,
RA	Rothenberg M.B., Stevens R.L.;
RT	"Tryptase 4," a new member of the chromosome 17 family of mouse serine proteases.";
RL	J. Biol. Chem. 276:20648-20658 (2001).
RN	[3]
RP	SEQUENCE OF 3-324 FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Testis;
RX	Medline=21085660; PubMed=112171851;
RA	Kawai J., Shinagawa K., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Araiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J.,
RA	Schnirli L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Wasilio T.,
RA	Salai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Query Match 30.8%; Score 530.5; DB 1; Length 275;

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OM protein - protein search, using sw model

Run on: August 29, 2002, 10:21:17 ; Search time 30.16 Seconds
 (without alignments)
 1818.282 Million cell updates/sec

Title: US-09-903-925A-263

Perfect score: 1720

Sequence: M V Y S G A P P A L G G C G C L G T F T S A Q G G G A L R A P S Q G S G A A R S 317

Scoring table: BLOSSUM62

Gapop 10.0 . Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 5622222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19;*

1: sp_archaea;*
 2: sp_bacteria;*
 3: sp_fungi;*
 4: sp_invertebrate;*
 5: sp_human;*
 6: sp_mammal;*
 7: sp_mnc;*
 8: sp_organelle;*
 9: sp_phage;*
 10: sp_plant;*
 11: sp_rabbit;*
 12: sp_virus;*
 13: sp_vertebrate;*
 14: sp_unclassified;*
 15: sp_rvirus;*
 16: sp_bacteriophage;*
 17: sp_archeap;*

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRIMER;	297 AA.
ID	088781			
AC	088781;			
DT	01-NOV-1998	(TREMBLrel	08,	Created)
DT	01-NOV-1998	(TREMBLrel	08,	Last sequence update)
DT	01-DEC-2001	(TREMBLrel	19,	Last annotation update)
DE		SERINE PROTEASE PRECURSOR (FRAGMENT).		
GN	BS22.			
OS	Rattus rattus (Black rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NCBI_TaxID	10117;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FISHER; TISSUE=BRAIN;			
RX	MEDLINE:98388725; PubMed=9722524;			
RA	Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe R.;			
RT	"Serine Proteases in Rodent Hippocampus.";			
RL	J. Biol. Chem. 273:2304-23011(1998).			
CC	-1 SIMILARITY: BELONGS TO PEPTIDE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.			
EMBL	AJ005642; CAA06644.1; -.			
DR	HSSP; P00763; 1DPO.			
DR	MEOPS; S01_252; -.			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR001254; Trypsin.			
DR	Pfam; PF00086; trypsin_1.			
DR	PRINTS; PRO0022; CHYMOTRYPSIN.			
DR	SMART; SM00020; TRYPSIN.			
DR	PROSITE; PS5240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	Hydrolase; Protease; Serine protease; Signal.			
FT	NON_TER	1		
FT	SIGNAL	<1		POTENTIAL.
FT	CHAIN	23		SERINE PROTEASE.
SEQUENCE	297 AA;	297		322086 MW;
				6DA25C6633DDAB55 CRC644;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1213.5	70.6	297	11	088781	rattus ratt
2	660.5	38.4	389	13	Q9PVX7	Q9PVX7 xenopus lae
3	603	35.1	317	13	Q9DR3	Q9DR3 xenopus lae
4	578.5	33.6	339	11	Q99144	Q99144 mus musculu
5	571	33.2	310	11	Q9IXC4	Q9IXC4 mus musculu
6	570	33.1	321	4	Q96RZ8	Q96RZ8 homo sapien
7	570	32.8	310	11	Q9QYZ9	Q9QYZ9 mus musculu
8	559.5	32.5	273	6	Q9XSM1	Q9XSM1 ovis aries
9	537	31.2	799	11	Q9DB10	Q9DB10 mus musculu
10	536	31.2	237	6	Q29464	Q29464 bos taurus
11	529.5	30.8	329	13	Q2272	Q2272 xenopus lae
12	524	30.5	273	11	Q921N4	Q921N4 mus musculu
13	517.5	30.1	275	4	Q96RZ6	Q96RZ6 homo sapien
14	491	28.5	806	6	Q18783	Q18783 macropus eu
15	485.5	28.2	279	11	Q99MS4	Q99MS4 mus musculu
16	480	27.9	282	11	Q9d4I3	Q9d4I3 mus musculu

Query Match	70.6%	Score 1213.5; DB 11; Length 297;	
Best Local Similarity	74.7%	Pred. No. 3e-104;	
Matches 222; Conservative 26; Mismatches 40; Indels 9; Gaps 1;			
Qy 6 APPAIGGGCTGTTTLLAATLNAATKIPVPPACKGKQQLNQVGGEDSTOSEWPNVY 65			
Db 5 SPPGL-----TLFILPSATVSAANIRGSPDCGGKQQLNQVGGEDSADAQWPNV 55			
Qy 66 SJQRNGTHHAGSLLTTSRVTIAAHCFKDNLNKFLPSVYLLGAWLGNGFGRSOKVGYAW 125			
Db 56 STLKNGSHHAGSLLTTSRVTIAAHCFKDNLNKFLPSVYLLGAWLGNGFGRSOKVGYAW 115			
Qy 126 VEPHPVSYNSKEGACADIALYRLERSQI OFFSERVLPICLDPDASTIHLPPNTCHWISGWGSIQD 185			
Db 116 VLPHPRYSKEGTHADIALYRLERSQI OFFSERVLPICLDPDASTIHLPPNTCHWISGWGSIQD 175			
Qy 186 GVPLPHPQTQLKVKPIIDSEVCSHLYRKGAGCOPITEDMLCAGLYLEGERDADLGDSGP 245			
Db 176 GVPLPHPQTQLKVKPIIDSEVCSHLYRKGAGCOPITEDMLCAGLYLESKRDACIGDSSGP 235			
Qy 246 LMCOVDGAMLLAGLISWGCAERNPVYISLSAHSRWSWEKTVQGVOLGRQAGGG 302			
Db 236 LMCOVDGAMLLAGLISWGCAERNPVYISLSAHSRWSWEKTVQGVOLGRQAGGG 292			
RESULT 2 Q9PWX7 ID Q9PWX7 PRELIMINARY; PRTR; 389 AA.			
AC O9PWX7; PRELIMINARY; PRTR; 389 AA.			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
GN XEPIPMSIN.			
OS Xenopus laevis (African clawed frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OC Xenopodinae; Xenopus.			
NCBI_TAXID=8355; RN [1]			
SEQUENCE FROM N.A.			
RA Yama da K.; The expression control of xepsin by non-axial and planar posteriorizing signals in Xenopus epidermis"; Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.			
RT -; SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYP SIN FAMILY.			
RL EMBL: AB018694; BAA84941.1; -.			
DR HSSP: P00763; IDPO.			
DR MEROPS: S01.048; -.			
DR InterPro: IPR01314; Chymotrypsin.			
DR InterPro: IPR01254; Trypsin.			
DR Pfam: PF00089; trypsin; 1			
DR PRINTS: PRO0172; CHYMOTRYPSIN.			
DR SMART: SM00020; TRYPSIN_SP_C; 1			
DR PROSITE: PS50240; TRYPSIN_DOM; 1.			
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR Hydrolase; Protease; Serine protease.			
DR HSSP: P00763; IDPO.			
DR MEROPS: S01.048; -.			
DR InterPro: IPR01314; Chymotrypsin.			
DR Pfam: PF00089; trypsin; 1			
DR PRINTS; PRO0172; CHYMOTRYPSIN.			
DR PROSITE; PS00020; TRYPSIN_DOM; 1.			
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR PROSITE; PS00135; TRYPSIN_SER; 1.			
KW Hydrolase; Protease; Serine protease.			
SEQUENCE 389 AA; 42375 MW; B31FB4A2F5D1F6E3 CRC64;			
Query Match 38.4%; Score 660.5;, DB 13; Length 389;			
Best Local Similarity 47.0%; Pred. No. 6.2e-53; Mismatches 95; Indels 11; Gaps 6;			
Matches 131; Conservative 42; Mismatches 95; Indels 11; Gaps 6;			
Qy 40 AGKPKOOLRVGGESTDSEMPWIVSIQKNGTHHAGSLTSRWTIAHCFKDNLNKP 99			
Db 16 AGCVPYTSNRVYGGMDSKRGEWPQIQLSLSKSDTGGSLTDTSWMTAHC1 -DSLDS 74			
Qy 100 YLFSLVLLGAWLGNGPGRSRQSKVGYAWVPEPHPVSNKEGACADIALYRLERSQFSEVL 159			
Query Match 38.4%; Score 660.5;, DB 13; Length 389;			
Best Local Similarity 47.0%; Pred. No. 6.2e-53; Mismatches 95; Indels 11; Gaps 6;			
Matches 131; Conservative 42; Mismatches 95; Indels 11; Gaps 6;			
Qy 40 AGKPKOOLRVGGESTDSEMPWIVSIQKNGTHHAGSLTSRWTIAHCFKDNLNKP 99			
Db 16 AGCVPYTSNRVYGGMDSKRGEWPQIQLSLSKSDTGGSLTDTSWMTAHC1 -DSLDS 74			
Qy 100 YLFSLVLLGAWLGNGPGRSRQSKVGYAWVPEPHPVSNKEGACADIALYRLERSQFSEVL 159			

Db	234	DSSGPLVKIQFWYQAGIVSNGERAQKRNPGVYTWPAYETWISE	280	RESULT 5
	Q99I44	PRELIMINARY;	PRT;	339 AA.
ID	Q99I44			
AC	Q99I44;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	SIMILAR TO PROTEASE, SERINE, 8 (PROSTASIN).			
GN	MUS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX				
[1]	NCBI_TAXID=10090;			
RN				
RP				
RA	Strausberg R.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDJB databases.			
RN				
RP				
RA	Strausberg R.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDJB databases.			
RN				
RP				
RA	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ, AND SWISS; TISSUE=LUNG;			
RA	Vergheze G.M., Caughey G.H.;			
RT	*Molecular cloning and characterization of mouse prostasin, a type I membrane-associated serine protease of the gamma-tryptase/prostasin gene family.;			
RT	Submitted (MAY-2001) to the EMBL/GenBank/DDJB databases.			
RL	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.			
CC	TRYPSIN FAMILY.			
DR	EMBL; BC003851; AAH03851.1;			
DR	EMBL; AF378086; AAH06320.1;			
DR	HSSP; P00734; IUVS.			
DR	MEROPS; S01_158;			
DR	InterPro; IPR001254; Trypsin.			
DR	Pfam; PF00089; trypsin_1.			
DR	PRINTS; PR00722; CHYMOTRYPIN.			
DR	SMART; SM00020; TRYSP_CPC;			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HHS; UNKNOWN_1.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	Hydrolase; Protease; Serine protease.			
SQ	SEQUENCE 339 AA;	36216 MW;	BC2DE88BC057AF10 CRC64;	
RESULT 6				
Q96RZ8				
ID	Q96RZ8			
AC	Q96RZ8;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	HS TRANSMEMBRANE TRYPSINE, GENE NAME TMT, AF175522_1.			
GN	TMT_P.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX				
[1]	NCBI_TAXID=9506;			
RN				
RP				
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=21096910; PubMed=11157797;			
RA	Daniles R.J., Peden C., Horsley S.W., Clark K., Tufarelli C., Kearney R., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.;			
RA	"Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";			
RT	Hum. Mol. Genet. 10:339-352(2001).			
RL	EMBL; AE006466; AAC61289.1;			
DR	Transmembrane.			
KW				
SQ	SEQUENCE 321 AA;	33829 MW;	FFF5089EDC4FC73D CRC64;	

Query Match	33.1%	Score 570; DB 4; Length 321;	
Best Local Similarity	41.1%	Pred. No. 1, 2e-44;	
Matches	123;	Conservative 44; Mismatches 108; Indels 24; Gaps 8;	
Db	3	LGAGLILLL--AVPGVSLRTPQPGGRQVSADGRTGVHAAAPGAWPQAISLR 59	
Qy	15	LGTFTSULLASTAILNRAPIVPPACGKPKQQLN--RVEGGEDSTDSEWPWIVS1OKNG 71	
Db	72	THHCAGSULTSRMVITAAHCFCNDLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 131	
Qy	60	VHVGCGSSLSPSWVLTAAHCFSGSLLNSSD--VQVHIGLETTLSLSPHET--VRQIILHS 115	
Db	132	YSWKEGACADIALVRLERSIQSERVLPICLPDASTHLPNTHCWCISGWGSTQDGVLPLPH 191	
Qy	116	PSGQPQTSGDIALVELSVPVTLSSRLPVCPLPEASDDFCGTRCWWTGWTREGEPLPP 175	
Qy	192	POTLOKUKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSSGPIAMQVD 251	
Db	176	PYSLREVKVSYVDTECRDY-PGPGGSILQPDMLCA--RSPGDAQCDDSGPLVCQN 231	
Qy	252	GAWLLAGLTSWQBGCAERNRPVAVYISLAHSWKEVITQGYOLRGRQGG--GAIRAP 307	
Db	232	GAWVQRTIVSNGECCGPRNPFGVYTRPVAYVWIRHII-----TASGGSESGYFRLP 283	
RESULT 7			
ID	Q9QYZ9	PRELIMINARY;	
AC	Q9QYZ9;	PRT;	
AC	Q9QYZ9;	310 AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
GN	DISP OR DISP.	DISTAL INTESTINAL SERINE PROTEASE.	
OS	Mus musculus (Mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10909;		
RN	[1]	SEQUENCE FROM N.A. MEDLINE=20246299; PubMed=10786627;	
RX		Shaw-Smith C.J., Coffey A.J., Leversha M., Freeman T.C., Bentley D.R., Walter J.R.;	
RA		"Characterization of a novel murine intestinal serine protease," DISP. ; R.	
RT		RL Biochim. Biophys. Acta 1490:131-136(2000).	
CC	-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRIPSIIN FAMILY.	
CC	CC	TRIPSIIN FAMILY.	
DR	AJ243866; CAB56465..1..	EMBL: AJ243866; CAB56465..1..	
DR	HSSP: P00763; 1DPO.	HSSP: P00763; 1AAO.	
DR	MEOPS: S01..04..2..	MEOPS: S01..04..5..	
DR	MGI: 133645;	MGI: 133645;	
DR	InterPro: IPR01314; Chymotrypsin.	InterPro: IPR01254; Trypsin.	
DR	InterPro: IPR01254; trypsin.	InterPro: IPR01254; Trypsin.	
DR	PRINTS: PR00089; trypsin.	PRINTS: PR00089; trypsin.	
DR	PFAM: PF00089; trypsin.	PFAM: PF00089; trypsin.	
DR	PROSITE: PS00020; TRYSP_CPC; 1.	PROSITE: PS00020; TRYSP_CPC; 1.	
DR	PROSITE: PS00022; CHYMOTRIPSIN.	PROSITE: PS00024; TRYPSIN_DOM; 1.	
DR	PROSITE: PS00072; TRYPSIN.	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.	
KW	Hydrolase; Protease; Serine protease.	Hydrolase; Serine protease.	
SEQUENCE	310 AA;	33701 MW;	
SQ	F828EC7FF6D25303F CRC64;	88A19DC779053898 CRC64;	
Query Match 32.8%; Score 564; DB 11; Length 310;			
Best Local Similarity	42.4%	Pred. No. 4e-44;	
Matches	117;	Conservative 48; Mismatches 95; Indels 16; Gaps 9;	
Db	1	LLLASTAILNRAPIVPPACGKPKQQLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 77	
Qy	21	LLLASTAILNRAPIVPPACGKPKQQLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 77	
Db	10	QILTRARDILPSLPSVGHSGRDKGIVGDALEQWQPMWVSLWTEDG-HICGG 65	
Query Match 32.5%; Score 559.5; DB 6; Length 273;			
Best Local Similarity	40.9%	Pred. No. 8.8e-15;	
Matches	113;	Conservative 53; Mismatches 95; Indels 15; Gaps 1;	
Db	2	LHLALALLSL--VSAAPGPGQALQSRSGIIGKEAGSRWPQVSLRVRDQYWRHQCGG 59	
Qy	21	LILLASTAILNRAPIVPPACGKPKQQLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 77	
Db	2	LILLASTAILNRAPIVPPACGKPKQQLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 77	
Qy	78	SLLTSRWVITAACFCFKONLNKPYLFSVLGAQWLNQPGRSQKVGVAYWEHPV 137	
Db	60	SLLHEWWVITAACFCFRRLSN-PSYYHVKGGLTLSLEPHSTLVAVRNIFVHPYLWADA 124	
Qy	138	ACADIALVRLERSIQSERVLPICLPDASTHLPNTHCWCNTSGMSIQDGVLPHPTQLOK 197	
Db	125	SSGGIALVQDTPRPSQ-FTPVCLPAACTPLPFGTVCNVTGATQE---RDMSVLO 180	
Qy	198	LKYPIDSEVCSHLY-WRG--AGOQGPITEDMLCAGYLEGERDACLGDSSGPIQVQDGA 253	
Db	181	LAVPLDSEDCERMYHTQCSSLSSTERLQSDMLCAGYVEGHIDSQGDSGPLYCSINSS 240	
Qy	254	WLLAGLISWNGEGCAERNREGVYISLARHSWKEV 289	
Db	241	WTQVIGTSMIGCARPYREGVYTRPVYDVIQRL 276	
RESULT 8			
Q9XSM1		PRELIMINARY;	
ID	Q9XSM1	PRT;	
AC	Q9XSM1;	273 AA.	
DT	01-NOV-1999	(TREMBLrel. 12, Created)	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	TRYPTASE (EC 3.4..21..59).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9440;		
RN	[1]	SEQUENCE FROM N.A. TISSUE=BONE MARROW. MEDLINE=2030142; PubMed=10848900; RA Scudamore C.L., Mcbue A.R., Huntley J.F., Collie D.D.S., Pemberton A.D., McAluese S.M., Huntley J.F., Miller H.R.P.; RT cDNA sequence of two sheep mast cell tryptases and differential expression of trypsin and sheep mast cell proteinase-1 in lung, dermis and gastrointestinal tract." Clin. Exp. Allergy 30:818-833(2000). RL Clin. EXP. ALLERGY 30:818-833(2000). CC -I SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRIPSIIN FAMILY. DR EMBL: Y18223; CAB:1988..1.. DR HSSP: P20231; 1AAO. DR SMART: SM00020; TRYSP_CPC; 1. DR MEROPS: S01..015.. DR InterPro: IPRO01314; Chymotrypsin. DR InterPro: IPRO01254; Trypsin. DR PFAM: PF00089; trypsin.1. DR PRINTS: PR00722; CHYMOTRIPSIN. DR SMART: SM00020; TRYSP_CPC; 1. DR PROSITE: PS50240; TRYPSIN_DOM; 1. DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1. DR PROSITE: PS00135; TRYPSIN_SER; 1. DR KW Hydrolase; Serine protease. FT CHAIN 29 273 AA; 30156 MW; 88A19DC779053898 CRC64; SQ SEQUENCE 273 AA;	Query Match 32.5%; Score 559.5; DB 6; Length 273; Best Local Similarity 40.9%; Pred. No. 8.8e-15; Matches 113; Conservative 53; Mismatches 95; Indels 15; Gaps 1;
Db	66	SLIHEWWVITAACFCFRRLSN-PSYYHVKGGLTLSLEPHSTLVAVRNIFVHPYLWADA 124	
Qy	138	ACADIALVRLERSIQSERVLPICLPDASTHLPNTHCWCNTSGMSIQDGVLPHPTQLOK 197	
Db	117	G-ADIALOLLEPVPSSCHYREVTLPPASETPPPGSCWVYWTGNGDNGRPPLPPYPIKO 175	

Qy	198	LKVPIIDSEVC SHLYWRGAGG--PIT-EDMILCAGYLEGERDACLGDGGPLMCQVYDGA	253	Best Local Similarity 40.7%; Pred. No. 4.e-41;
Db	176	VKPIVENSVCWRYHSGLSTYSVPIQEDILCAG--DGGRDSCCGDSSGGFLVKVNGT	233	Matches 103; Conservative 54; Mismatches 82; Indels 14; Gaps 6;
Qy	254	WLLAGLISWGECAERNRPGVYIISLAHRSWEKIV	289	QY 41 CGRQQUNRVGGEDSTSEWWNIVSIOQKNGTHCAGSLLTSRWVTAAHCF-KDNLNKP 99
Db	234	WLQAGVYWSWGDCANPDYGPYTRITSYLDNHQYY	269	Db 556 CGLQGLESSRIVGTVSSEGWPAQSLQIRGHICGALIADRWTAAHCQFQEDSNASP 615
RESULT	9	Q9DBB0 PRELIMINARY; PRT; 799 AA.		QY 100 YLFSLVLLGAWOLGN-PGSRSQLKVGVAWEHPVYSKEGACADIALVRLERSIQFSERV 157
Q9DBB0	ID			Db 616 KLTWTFGLKMRNSRWPGEVSKVSRSLFLHPP--YHEDSHYDVALLQDIPVVISATV 672
AC	Q9DBB0;			QY 158 LPICLCPDASIHLEPPNTQWISGMGSIODGVPLPHPTQLKVPILDSEVCSHLYWRGAG 217
DT	01-JUN-2001	(TREMBLrel. 17, Created)		Db 673 REVCLPARSHFFEPGQHQWITGWAQOREGGPSN-TLKQVVDVLVPDLCSEAY ---- 725
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		QY 218 QSPITEDMLCAGYLEGEDDACIJDGSGGFLMC-QVDGAWLACTISRGCAIRNRPEVYI 276
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		Db 726 RYQVSPSPMLCAGYRKGKDKACQGDSSGGFLVCREPSGRWFLAGLVSMGLGCRPNFFGVYT 785
OS	Mus musculus (Mouse).			QY 277 SLSAHSRSWEEKLV 289
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			Db 786 RVTRVNWIQQVL 798
NCBI_TAXID=10090;				
RN	[1]			
RP	SEQUENCE FROM N_A.		RESULT 10	
RC	SEQUENCE STRAIN=C57BL/6J; TISSUE=LIVER;		ID Q29464 PRELIMINARY;	PRT; 237 AA.
RX	MEDLINE=21085660; Published=11217851;		AC Q29464;	
RA	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Boni H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kihara P., Lewis S., Matsuo Y., Nikaido I., Pessie G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mazzarella J., Mombretti P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-F., Suzuki H., Toto-oka K., Wang H., Weitz C., Whittaker C., Wilming L., Wyrshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;		DT 01-NOV-1996 (TREMBLrel. 01, Created)	
RA	Functional annotation of a full-length mouse cDNA collection. ; Nature 409:655-650 (2001).		DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.		DE TRYPTASE (EC 3.4.21.59) (FRAGMENT).	
DR	HSSP; P00763; 1DPQ.		OS Bos taurus (Bovine).	
DR	MGD; MG1:191903; 1300008A2Rik.		OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Bos.	
DR	InterPro; IPR001314; Chymotrypsin.		NCBI_TAXID=9013;	
DR	InterPro; IPR000559; CUB.		RN [1]	
DR	InterPro; IPR002172; LDL_recept_A.		RP SEQUENCE FROM N_A.	
DR	IPR001234; Trypsin.		TISSUE=LIVER CAPSULE;	
DR	Pfam; PF00057; IgI_recept_A.		RC MEDLINE=96203914; Published=8620861;	
DR	Pfam; PF00089; trypsin.		RA Pallaoro M., Gambacurta A., Fiorucci L., Mignogna G., Barra D., Ascoli F.;	
DR	PRINTS; PRO0022; CHYMOTRYPTIN.		RA RT	
DR	SMART; SM00020; TRYSP_CPC_1.		RT cDNA cloning and primary structure of trypsinase from bovine mast cells and evidence of the expression of bovine pancreatic trypsin inhibitor mRNA in the same cell. ;	
DR	PROSITE; PS5240; TRYSP_DOM; 1.		RT Eur. J. Biochem. 237:100-105 (1996).	
DR	PROSITE; PS00134; TRYSPN_HIS; UNKNOWN_1.		RL CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.	
DR	Hydrolase; Serine protease.		CC DR EMBL; P20231; CA64438..1; -.	
FT	NON_TER		DR HSSP; P20231; 1AAO.	
SQ	SEQUENCE 237 AA; 26550 MW;		DR InterPro; IPR001314; Chymotrypsin.	
Query Match	31.28;	Score 537; DB 11; Length 799;	DR InterPro; IPR001254; Trypsin.	
Query	198		DR Pfam; PF00089; trypsin.	
Query Match	31.28;	Score 536; DB 6; Length 237;	DR PRINTS; PRO0022; CHYMOTRYPTIN.	
Query	59	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR Glycoprotein Hydrolase; Serine protease.	
Db	2	Score 537; DB 11; Length 799;	DR SMART; SM00042; CUB; 1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR PROSITE; PS50068; LDLRA_2; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
Db	2	Score 536; DB 6; Length 237;	DR PROSITE; PS000261; LDLRECEPTOR.	
Db	2	Best Local Similarity 42.6%; Pred. No. 1.e-41;	DR SMART; SM00192; CDDA; 3.	
Db	2	Matches 103; Conservative 48; Mismatches 75; Indels 16; Gaps 7;	DR PROSITE; SM00020; TRYSP_CPC_1.	
Db	2	Score 537; DB 11; Length 799;	DR PROSITE; PS00180; CUB; 1.	

Db	59	YDQOLPISRITPHPNCSVKNK-ADIALELDKLVNISHWYQPVTLPPESETFPFGTQ	116	Db	177	NVKIISROTNCNLHYHINPSSDSLGSVQODMICAGSAAGSVDAQCQGDSGGPLTCVNINQPY	236
Qy	175	CWISWGGSITQDGVLPHFQTLQKUKVPTIDSECVCSHLYWRGAGQP---TIEDMLCAGY	230	Oy	256	LAGTISNGECAERNPQGVYISLSAHSRWEKI	288
Db	117	CWTFGWGNNDNGRRLRPPPFKQKVPKVPEVNSYCDKXHSGLSTGDNVPIREDMLCAG-	175	Db	237	LAAVVSNGDECAGAPNRPGVYILSYYSWIRSI	269
Qy	231	LEGERDACLGDSGGPLMCGQVDGAWLLAGTISNGECAERNPQGVYISLSAHSRWEKI	289	RESULT 12			
Db	176	-DSGRNFCCGDSGGPLVCKVNGTWLQAGVVSNGDCAKPNRPGIYTRVTSYLDWIHQVP	234	0921N4	PRELIMINARY;	PRT;	273 AA.
Qy	290	QG 291		ID Q921N4			
Db	235	QG 236		AC Q921N4;			
RESULT 11				DT 01-DEC-2001 (TREMBLrel. 19, Created)			
ID 042272	PRELIMINARY;	PRT;	329 AA.	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
AC 042272;1				DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DT 01-JAN-1998 (TREMBLrel. 05, Created)				DE MAST CELL PROTEASE 7.			
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)				OS Mus musculus (Mouse).			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DE SERINE PROTEASE.				OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
GN CAPI.				RN [1]	SEQUENCE FROM N.A.		
OS Xenopus laevis (African clawed frog).				RA Strausberg R.;			
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;				RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.			
OC Xenopodinae; Xenopus.				DR EMBL; BC011328; AAH1128.1; -.			
OX				KW Protease.			
RN [1]	SEQUENCE FROM N.A.			SQ SEQUENCE 273 AA; 30332 MW; 51417476514035BE CRC64;			
RC TISSUE=EPITHELIUM;				Query Match 30.5%; Score 524; DB 11; Length 273;			
RX MED-974477; Published=9335501;				Best Local Similarity 38.1%; Pred. No. 1.7e-40;			
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;				Matches 109; Conservative 55; Mismatches 84; Indels 38; Gaps 9;			
RT "An epithelial serine protease activates the amiloride-sensitive				Qy 22 LLLASTAILNAARIPVPPACGKPKQLNRRVGGEDSTSEWPNTVSKNGT--HHQAGS 78			
PT serine channel.";				Db 4 LLLTLPILLSSLYAAP--GPAMTRGIVGQEAHNGKWPQVSLLRANTYWMHFCGGS 60			
RL Nature 389:607-610(1997).				Qy 79 LLTSRWVITAHC-----FKDNLNKPFLPSVLLGAQOLGNPGRSRQKVGAYPEP 128			
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE				Db 61 LJHPQWVITAARCVGPDPADPNKVRQVLRQKQVY-----YHDHLMTVSDIT 107			
CC TRYPSIN FAMILY.				Qy 129 HP-VYSNKEGACADIALVRLERSIOFSERVLPICLPDASILHPPNTICWISGWGSIQDG 187			
CC EMBL: AF029404; AAB96905.1; -.				Db 108 HPDFYTVQDG--ADIALKLTKTPVNISDVYHVPVLPASETPSGTLCWVTCWGNITNGV 165			
DR HSSP; P00763; 1DPO.				Qy 188 PLPHPQTFLQRKLPVPIISeVCVSHLYWRGAGQQP---LTEDMCAGYLGERDACLDSG 243			
DR "An epithelial serine protease activates the amiloride-sensitive				Db 166 NLPPPFFPLIKEQVQPIIENHLCDKLYHRGLITQDNNVHVRDDMUCAGN-EG-HDSCQGDSG 223			
PT serine channel.";				Qy 244 GPLMCQYDGAWLLAGISWSGECAERNPQGYITSLSAHRSWEKIY 289			
RT InterPro: IPR001314; Chymotrypsin.				Db 224 GPLVCKYEDTWILOGVTSWGEQAQPQRPGITRVTYLDWTHRYV 269			
DR InterPro: IPR01254; Trypsin.				RESULT 13			
DR PTfan; PP00083; trypsin; 1.				Q96RZ6 PRELIMINARY; PRT; 275 AA.			
DR SMART; SM00300; TRYSPC; 1.				ID Q96RZ6			
DR PROSITE: PS50240; TRYPSIN_DOM; 1.				AC Q96RZ6;			
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.				DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DR PROSITE: PS00135; TRYPSIN_SER; 1.				DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DR HYDROLASE; Protease; Serine protease.				DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;				DE TRYPTASE I.			
RC TISSUE=EPITHELIUM;				GN TRYPTASEC.			
RX MED-974477; Published=9335501;				OS Homo sapiens (Human).			
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RT "An epithelial serine protease activates the amiloride-sensitive				OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
PT serine channel.";				RN [1]	SEQUENCE FROM N.A.		
RL Nature 389:607-610(1997).				RP MEDLINE-2106910; PubMed-11157797;			
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE				RX RA Tufarelli C., Kearney L., Buckle V.J., Flint J., Higgs D.R.;			
CC TRYPSIN FAMILY.				RA *Sequence, structure and pathology of the fully annotated terminal 2			
CC EMBL: AF029404; AAB96905.1; -.				RT			
DR HSSP; P00763; 1DPO.							
DR "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
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RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
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DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
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Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
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RT InterPro: IPR001314; Chymotrypsin.							
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DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
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RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							
DR SMART; SM00300; TRYSPC; 1.							
DR PROSITE: PS50240; TRYPSIN_DOM; 1.							
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR HYDROLASE; Protease; Serine protease.							
KW SEQUENCE 329 AA; 35276 MW; 71D1D556EB09A8E0 CRC64;							
RC TISSUE=EPITHELIUM;							
RX MED-974477; Published=9335501;							
Vallet V, Chraibi A., Gaegeler H.P., Horisberger J.D., Rossier B.C.;							
RT "An epithelial serine protease activates the amiloride-sensitive							
PT serine channel.";							
RT InterPro: IPR001314; Chymotrypsin.							
DR InterPro: IPR01254; Trypsin.							
DR PTfan; PP00083; trypsin; 1.							

RT	Mb of the short arm of human chromosome 16. ";	KW	Hydrolase; Serine protease.
RL	Hum. Mol. Genet. 10:339-352(2001).	SEQUENCE	806 AA; 9081 MW; 95FAA86DC20064D5 CRC64;
DR	AE006466; AAK61271.1;	SQ	SEQUENCE 275 AA; 30601 MW; 2F4AAAE7DDE483E CRC64;
SG			
Query Match	Score 517.5; DB 4; Length 275;	Score 491; DB 6; Length 806;	
Best Local Similarity	30.1%; Pred. No. 6.9e-40;	Best Local Similarity	28.5%; Pred. No. 7.4e-37;
Matches	52; Mismatches 88; Indels 37; Gaps 9;	Matches	99; Conservative 50; Mismatches 86; Indels 22; Gaps 7;
QY	20 SILLASTAILNARIAIRIPVPPACGKRPQQLNRVYGGEDSTDSEPNPVIQSQTKNG -- -THHCA 76	QY	41 CGKPQQ---LNRVVGDEDSTDSEPNPIVSIQ KNGTHHCAGSLLTTSRWVITAHCFLD 94
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:	Db	563 CGPRVEPKCPGRIVGGCYAQPHSWPQISLSTRFGEEFCGGTLIAQWVLTAAHCL-E 621
QY	77 GSILTSRNVITAHC---FKD-----NLNPYLFVSLVLLGAQWLGNGPSRSOKVGYAW 126	QY	95 NLNKPYLFSVLLGAQWLGNGPSRSOKVGYAWVEPHPVYSWKEGACADALVRLERSIERS 154
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:	Db	622 RSQWPAGAVKVLGLHLREVNPESTSQEIGSYSLRFKGPL-----AADALIKLNRPAIN 674
QY	61 GLS1HPOQWLTAACVGPDKDIAALRQLREQHLY-----YQDQLLPVSR1 107	QY	155 ERLVPLCPLPDASTHLPNPTNHCWISGWGSTQDGYPPLPHOTOLKLKVPLIDSEYCS-HLYW 213
QY	127 EPLP-VYNSKEGACADIALVRLESIOSERVATPICLDASITHLPNPTNHCWISGWGSTQD 185	Db	675 DKVTPACPLPSQDFMNPVDPFLCHVIGWDQTGTSP---EGLLKQASLPVTDNRYCNRHEVL 731
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:	QY	214 RGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVNGAWLLAGIISWEGCAERNRPG 273
QY	108 IVHQFQYTAQIG--ADIALLEELEPVANVSSHVHTVTPPASETFPPGMPCWVTCGWGDVDN 165	Db	732 NGR---VKSTELCAGHLVGRGDSQCGSGGPLICEFDKDYKVLOGVTSWGLGCARPNNRPG 787
QY	186 GVLPLPHPQTLQKLKVPLIDSEYCSHLYWRGAGQGP---ITEDMLCAGYLEGERDACLGD 241	QY	274 VYTSLSUHSWSWKEIVQ 290
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:	Db	788 VYVRSVRYLSWIEDVMK 804
QY	166' DERIPLPFPLQKVPIMENHICDAKYHIGATYGDVDRIDMLCAG--NTRRDSQCGD 223		
QY	242 SGGPLMCQVDGAWNLAGLISWEGCAERNPGYVYISLSAHRSHWEKIV 289		
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:		
QY	224 SGGPLVCKYNTW1QAGYVWRGECAQPNPGTYTRYTYYLDTWTHXXV 271		
Db	:11111 :1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:1111:1:		
RESULT	15	RESULT	15
Q99MS4	PRELIMINARY;	Q99MS4	PRELIMINARY;
ID	Q99MS4	ID	Q99MS4
AC	Q99MS4	AC	Q99MS4
DT	01-JUN-2001 (TREMBLel 17, Created)	DT	01-OCT-2001 (TREMBLel 18, Last sequence update)
DT	01-OCT-2001 (TREMBLel 18, Last sequence update)	DT	01-OCT-2001 (TREMBLel 19, Last annotation update)
DT	01-DIC-2001 (TREMBLel 19, Last annotation update)	GN	IMPLANTATION SERINE PROTEINASE 2.
DE	PLASMINOCEN.	OS	Mus musculus (Mouse).
OS	Macropus eugenii (Tammar wallaby).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
NCBI_TaxID	9315;	NCBI_TaxID	10090;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
TISSUE-LIVER;		RX	MEDLINE=21361749; PubMed=1146794;
RX	LINE=21361749; PubMed=1146794;	RA	O'Sullivan C.M., Liu S.Y., Rancourt S.I., Rancourt D.B.;
AC	LINE=21361749; PubMed=1146794;	RT	"Regulation of the trypsin related proteinase ISP by progesterone in
DT	01-JAN-1998 (TREMBLel 05, Created)	RT	endometrial gland epithelium during implantation in mice.";
DT	01-JAN-1998 (TREMBLel 05, Last sequence update)	DE	Reproduction 122:235-244 (2001).
DT	01-DIC-2001 (TREMBLel 19, Last annotation update)	GN	-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
DE	PLASMINOCEN.	CC	TRYPSIN FAMILY.
OS	Macropus eugenii (Tammar wallaby).	CC	EMBL / AP05125; AAC15264.2; - .
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	HSSP; P00763; 1DPO.
NCBI_TaxID	9315;	DR	MGD; MGI:2149932; ISP2.
RN	[1]	DR	InterPro; IPR001314; Chymotrypsin.
RP	SEQUENCE FROM N.A.	DR	InterPro; IPR001254; Trypsin.
RT	LINE=21361749; PubMed=1146794;	DR	PRINTS; PRO0722; CHYMOTRYPSIN.
RA	LINE=21361749; PubMed=1146794;	DR	PROSITE; PS5040; TRYPSIN_DOM; 1.
RT	LINE=21361749; PubMed=1146794;	DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
RL	LINE=21361749; PubMed=1146794;	DR	PROSITE; PS00135; TRYPSIN_SER; 1.
CC	-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE	DR	KW Hydrolase; Serine protease.
CC	TRYPSIN FAMILY.	SQ	SEQUENCE 279 AA; 30986 MW; 81C43A59935244D7 CRC64;
DR	EMBL / AF05125; AAC15264.2; - .	Query Match	28.2%; Score 485.5; DB 11; Length 279;
DR	HSSP; P00747; 5HPG.	Best Local Similarity	36.5%; Pred. No. 6.4e-37;
DR	MEPROS_S01_223;	Matches	103; Conservative 53; Mismatches 107; Indels 19; Gaps 7;
DR	InterPro; IPR001314; Chymotrypsin.	QY	21 LLIUASTA1LNAAARIPIPAPCGKPOQLNRYVGGEDSTDSEWPWIVSIO----KNGTHH 74
DR	InterPro; IPR001314; Chymotrypsin.	Db	2 LIQLCLTFLFLGCSJAGTAPGPDVLMGIVGGHSAPQRKWPVOSLR1IYRYWAFWWVN 61
DR	InterPro; IPR001254; Trypsin.	QY	75 CAGSLLTTSRWVITAACFKDNLNKPYLFSVLL-AWQLGNPGSRQSKVGVAYWEPHPVYS 133

Db	62	CGGSITIHPDWLTAHCRLTRDAEFSVERTRGEAFLYGG---KELLSVSRVTHIPDFV	117
Qy	134	WKEGACADIALVRLERSIQFSEVRVLPICLPDASITHLPPNTNHCWISGWGSTODGYPLPHHQ	193
Db	118	-HAGGSIDVALLOLAIVSYOSFPNTPKVLPSESEVTKRDVCWYGAVSTHSRLPPX	176
Qy	194	TLOKLKVPIIDSEVNSHLY---WRGAQGPTEDMLCAGYLEGDRDACLGDGGPLMC	248
Db	177	RQQVKKIDNSLCEEMYHNATRHRNRGQKLKDMCLAGN-QG-Q-DSCYGDGGPLVC	234
Qy	249	QVDQAWLILAGLISMGCGCAERNPGVVYISLSAIRSWVERKIVQ	290
Db	235	NYTGWSLWTLLVGVSSWNGCGCAARDFGGYXARVOSPLWITOCMO	276

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Job time: 253 sec